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(54) **Assay method utilizing polynucleotide sequences.**

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Description

The present invention relates to assays, both immunoassays and nucleic acid assays of analytes, which utilize a universal detection system based on polynucleotide interactions.

The analysis and detection of minute quantities of substances in biological and non-biological samples has become a routine practice in clinical and analytical laboratories around the world. Broadly, the analytical techniques can be divided into those based on ligand-receptor interactions (e.g., immunoassay-based techniques), and those based on nucleic acid hybridization (polynucleotide sequence-based techniques).

For example, immunoassay techniques involve, at some stage or step in the process, the non-covalent association between an antibody binding site and an antigen complementary therefor. See, for example, "An Introduction to Radioimmunoassay and Related Techniques" by T. Chard, North Holland Publishing Company, Amsterdam, New York, Oxford, 1978. In polynucleotide sequence-based techniques, the process, at some step or another, involves the non-covalent binding of a polynucleotide sequence to a complementary sequence under hybridization conditions. (See for example, Falkow et al, U.S. Patent 4,358,535, Wahl et al, U.S. Patent 4,302,204, and Heimer, U.S. Patent 3,755,086.)

EP-A-0 124 221 which is a document according to Art. 54(3) and (4) EPC discloses a diagnostic method involving the binding of 3 entities to form a complex, followed by the detection of the signal whereby the three entities are the following:

(1) the analyte, i.e., a nucleotide sequence to be detected;

(2) a bridging entity comprising a nucleic acid sequence complementary to that which is to be detected and a polynucleotide tail, preferably a poly d(A)- or poly (dT)-tail and

(3) a signal entity or marker comprising a polynucleotide capable of complexing to the polynucleotide portion of said bridging entity and a signal generating portion wherein an enzyme (HRPO) is attached to a single stranded portion of the polynucleotide.

In a generalized sense, both the aforementioned techniques involve a primary recognition event, brought about by precise molecular alignment and interaction, and energetically favored by the release of non-covalent bonding free energy (e.g., hydrogen bonding, dispersion bonding, ionic bonding, dipolar bonding, and the like). In addition to the primary recognition event, both techniques also involve, at one step or another, a signalling event. This step or event relates to the necessity of detecting, in some demonstrable manner to a human or instrument detection system, the primary recognition event.

Signalling has been centered mainly in two broad areas: radioactive and non-radioactive techniques. Radioactive signalling has relied on radiolabeling of one or more components involved in the system, with such atoms as ^{32}P, ^{131}I, ^{14}C, ^{3}H, and the like. Detection is usually by means of a radioactivity detector. Non-radioactive techniques have been increasingly used in the last few years, since they involve no radioactivity, thus making such techniques safer, cleaner and more stable towards storage. They have been developed to sensitivities as high if not higher than radiolabeling techniques. Among the most common non-radioactive signalling techniques used at present are enzyme linked immunoassays (see, for example, Schuurs, A.H. et al, Clinica Chimica Acta, 81: 1-40 (1977)), fluorescence (Bauman et al, Chromosoma, 84: 1-18 (1981)), indirect immunofluorescence (Rudkin et al, Nature, 265: 472-473 (1977)), avidin-biotin interactions (Manning, J, et al, Biochemistry, 16: 1365-1370 (1977)), electron microscopy of electron dense nuclei such as ferritin (Broker, T.R. et al, Nucleic Acids Research 5: 363-384 (1978)), latex attachment (Sodja, A., ibid 35: 385-401 (1978)), combinations of the aforementioned techniques, and others.

The primary recognition event and the signalling event need to be coupled to each other, directly or indirectly, proportionately or inversely proportionately. Thus, in such systems as nucleic acid hybridizations with radiolabeled probes, the amount of radioactivity is usually directly proportional to the amount of analyte present. The same is true with a system such as a sandwich immunoassay, wherein the amount of labeled second antibody being detected is normally directly proportional to the amount of antigen present in the sample. Inversely proportional techniques include, for example, competitive immunoassays, wherein the amount of detected signal decreases the more analyte present in the sample.

The prior art has also utilized amplification techniques, wherein the signalling event is related to the primary recognition event in a ratio greater than 1:1. Thus, the signalling component of the assay may be present in a ratio of 10:1 to each recognition component, thereby providing a 10-fold increase in sensitivity.

The great versatility of polynucleotide sequence-based recognition systems has caused an extensive amount of experimentation and research to be invested therein. This versatility is brought about by the precise alignment of complementary nucleotide bases to each other, adenine (A) aligning to thymidine (T) and guanine aligning with cytidine (C). Given this complementarity, it is possible to utilize any desired sequence to provide an infinitely versatile system.

One of the impediments to a more extensive use of polynucleotide interaction-based systems, however, has been the necessity of attaching signalling or reporter groups (such as radioactive phosphorous, or enzymes, or biotin, or the like) to individual nucleotide

residues in the polymer chain. At least two problems arise out of this requirement.

First, the chemical reaction conditions involved in the modification of a polynucleotide polymer are generally too vigorous to be sufficiently selective for any one nucleotide in particular. For example, dicarbonyl reagents such as kethoxal or glyoxal will indiscriminately react with guanine (see for example Shapiro, R. et al, Biochemistry, 5: 2799-2807 (1966), Litt, M, ibid, 8: 3249-3253 (1969), or Politz, S.M. et al, ibid, 20: 372-378 (1981)). Thus, if one were to use a dicarbonyl-based cross-linking agent to attach an enzyme or a low molecular signalling compound directly on a polynucleotide chain, one would risk (and in fact one obtains) modification of a substantial amount of all guanine residues in the chain. This, of course, severely hinders the use of such modified chain in a recognition step. This problem has been solved in the prior art by the use of enzymatic (DNA polymerase-based) incorporation of individual modified nucleotides (previously modified in a non-hydrogen-bond-disruptive manner) into a nascent polynucleotide chain. It would, however, be preferred to utilize chemical modification techniques on the final polynucleotide polymer itself.

A second problem is associated with the attachment of signalling groups to polynucleotides and is somewhat related to the first. The problem is based on the necessity of synthesizing, by sometimes sophisticated and elaborate synthetic techniques, the modified monomeric nucleotide units themselves, prior to their enzymatic incorporation into polymer. Thus, radiolabeled nucleotides or biotin-labelled nucleotides have to be independently synthesized. Further, the amount of incorporation of a chemically modified nucleotide into final nucleic acid polymer may also influence the ability of a probe to recognize a given sequence on the analyte. This is particularly important if amplification techniques are utilized wherein signalling groups greatly outnumber recognition groups.

It would therefore be very useful to develop an assay system which utilizes components that are easily prepared, amenable to chemical modification rather than enzymatic-based reactions, that would utilize the great versatility of polynucleotide-based sequence recognition, and include the possibility of signal amplification methods.

The present invention provides a universal assay system which takes advantage of polynucleotide sequence recognitions, which allows for the use of chemical modification reactions, which is also capable of utilizing recognition events based on any type of non-bonding interaction, and which can use any of the myriad of available signalling methods.

The process of the invention comprises a method of detecting in a sample an analyte (A) having a molecularly recognizable portion thereon, which comprises:

forming a complex comprising (1) said analyte bound to (2) a molecular bridging entity comprising a portion capable of recognizing and binding to said molecularly recognizable analyte portion, and a portion comprising a polynucleotide sequence; and (3) a signalling entity comprising a recognition portion capable of complexing to said polynucleotide portion of said bridging entity, and a signal generating portion; and

detecting a signal provided by said signal generating portion present in said complex.

The invention provides, in addition to the aforementioned process, various elements and components to be used therein, such as various molecular bridging entities, and various signalling entities, as well as kits comprising said entities, and other components for use in the process.

In essence, the invention is based on the realization that the recognition portion and the signalling portion of the multi-component assay system should be present on different components of the system, thereby separating them, and avoiding the interference of the signalling portion on the recognition portion. This separation into multi-component entities, also allows the signalling portion to be attached to one of the components by chemical modification techniques, without affecting the recognition component.

Uses for the process, system and components are unlimited, and include all of the uses to which prior art assay techniques have been put, as well as generally, the detection of any analyte capable of recognition, in any sample.

BRIEF DESCRIPTION OF THE FIGURES

The invention will be better understood by reference to the attached Figures wherein:

FIGURE 1 represents a generalized scheme for the assay system of the invention. Analyte 1, having a molecularly recognizable portion 2 thereon, is brought into contact with molecular bridging entity 3, having a portion 4 thereon capable of recognizing the molecularly recognizable portion 2 on analyte 1. Bridging entity 3, in addition, carries a portion 5 comprising a polynucleotide sequence, generally denoted as ATCGATC... . Also present in the system is signalling entity 6 having thereon a polynucleotide portion 7 capable of annealing to polynucleotide portion 5 of the bridging entity 3. The signalling entity 6 also carries a signal generating portion 8. When analyte is present in the sample being analyzed, interaction occurs with bridging entity 3 through the recognizable and recognition portions 2 and 4, respectively. The complex formed thereby is then annealed through the polynucleotide portion 5 to the complementary polynucleotide portion 7 on the signalling entity, which brings the signalling portion 8 into some stoichiomet-

ric relation with the analyt 1.

FIGURE 2 shows a preferr d system und r the broader concept of the invention, wherein analyte 9 comprises a DNA sequence 10 (generally indicat d as ATCGATCGATC). Bridging entity 11, shown as a single-stranded circular polynucleotide polymer, carries a recognizing portion 12 which is a DNA sequence complementary to the DNA sequence of the analyte. Bridging entity 11 also carries, in addition, a poly G sequence 13, which is capable of annealing and forming a stable hybrid with complementary poly C sequence 15 on signalling entity 14. Signalling entity 14 also carries a biotin portion 16 as its signal generating group. Presence of the DNA sequence 10 in the sample being analyzed causes the bridging entity 11 to hybridize thereto, and subsequent annealing of the signalling entity to the thus formed complex attaches the biotin portion, through the network, to the analyte. The biotin portion 16 can then be detected, for example by addition of an avidin/enzyme couple, followed by addition of enzyme substrate, and color detection.

SYSTEM COMPONENTS

The term "analyte" as used in the specification and claims includes any substance or substances either alone or in admixtures, which presence is to be detected and, if necessary, quantitated. The analyte may be a molecule of small or high molecular weight, a molecular complex, or a biological system, such as a virus, a cell, or group of cells. Among the common analytes are proteins, polysaccharides, lipopolysaccharides, protein complexes, nucleic acids or segments thereof, either single- or double-stranded, whole viruses or viral components such as cores or capsids, bacteria of various different types, tissue cells, and the like. Among the most common proteins are the structural proteins, enzymes, immunoglobulins, or fragments thereof. Among the most common nucleic acids are DNA and RNA of various different types, such as tRNA, mRNA, rRNA, and the like. Bacteria, either whole or fragments thereof, such as cell walls or other recognizable portions, include both gram positive and gram negative bacteria. Fungii, algae, and other submicroscopic microorganisms are also included, as well as animal (e.g., mammalian) cells.

The analyte should have a "molecularly recognizable portion" thereon. This phrase denotes any molecular portion of the analyte which is capable of being recognized by a complementary molecular portion on the bridging entity of th system. Molecular recognition, as will be understood by thos of skill in the art, includes the non-covalent binding in thre dimensions b twe n complementary portions of two molecules. A molecularly recognizable portion on an analyte may be, for xample, a polynucleotid sequence, such as RNA or DNA, to b r cogniz d by its complem ntary sequence; an antig n portion, to be recognized by its corresponding monoclonal or polyclonal antibody; an antibody portion, to be recognized by its corresponding antigen; a l ctin portion, to be recognized by its sugar; a sugar portion, to be recognized by its lectin; a hormone portion, to be recognized by its receptor; a receptor portion, to be recognized by its hormone; an inhibitor portion, to be recognized by its enzyme; an enzyme portion, to be recognized by its inhibitor; a cofactor portion, to be recognized by a cofactor enzyme binding site; a cofactor enzyme binding site portion, to recognized by its cofactor; binding ligand recognized by its substrate and vice versa (i. . biotin-avidin); or any permutation or combinations thereof.

Among the most common molecularly recognizable portions are the three-dimensional protein arrangements in antigens of various different sorts, the cell wall structures present in various cells, or the nucleic acid sequences present in the DNA or RNA of organisms.

The second component of the system is the "molecular bridging entity". This entity need only contain a first portion capable of recognizing the molecularly recognizable portion on the analyte, and a second portion which comprises a polynucleotide sequence. These two portions of the bridging entity may be of the same type (i.e., both of them polynucleotide s - quences, albeit different ones) or of a different type (one being, for example, an antibody portion and the other the polynucleotide portion.)

The portion on the bridging entity capable of recognizing the molecularly recognizable portion on the analyte must contain a molecule or molecular fragment complementary to the recognizable portion on the analyte. Therefore, if the analyte contains a polynucleotide sequence, the recognizing portion of th bridging entity should be a complementary polynucleotide sequence or "probe". If the molecularly recognizable portion on the analyte is a generalized antigen, the recognizing portion on the bridging entity should be an antibody thereto. The same is true with respect to the complementary pairs sugar/lectin, receptor/hormone, inhibitor/enzyme, and the like, described previously.

The second portion of the molecular bridging entity must comprise a polynucleotide sequence. The polynucleotide sequence can be any chosen sequence, provided that it is long enough to provide stable annealing with a complementary sequence under given stringency conditions, that it be complementary to the polynucleotide sequence on the signalling entity, and, if th recognizing portion on the bridging entity is its lf a polynucleotid sequence, that it b suffici ntly different from said recognizing sequenc portion, to avoid hybrid formation betw n the analyt sequ nce and the second polynucleotide portion

on the bridging entity. The latter of the three conditions is required to prevent molecular confusion with concommitant appearance of false results.

The second portion polynucleotide sequence on the bridging entity (i.e., the one complimentary to the sequence on the signalling entity) may code for a particular gene product or products, or may code for no gene product at all. Thus, any structural gene or portion thereof could be used as the polynucleotide sequence portion on the bridging entity. A preferred sequence, however, would not code for a given gene since such coding may interfere with complementary gene sequences present in the analyte. It is thus preferred to choose polynucleotide sequence portions on the bridging entity which are non-coding, and not likely to be complementary to sequences on the analyte such as, for example, sequences comprising poly deoxy G, poly deoxy A, poly deoxy GT, poly deoxy GA, poly deoxy GAT, poly deoxy GTA, or any other low complexity (repeating) sequence. By "polynucleotide" is meant to include both polyribonucleotides, polydeoxyribonucleotides, or any poly-purine, -pyrimidine or analog and combinations thereof.

Specific examples of bridging entities as used in this invention are covalently attached entities of monoclonal or polyclonal antibodies with polynucleotides, polynucleotides with polynucleotides, protein antigens with polynucleotides, saccharides with polynucleotides, small molecular weight organic compounds with polynucleotides, lectins with polynucleotides, receptors with polynucleotides, hormones with polynucleotides, enzyme inhibitors with polynucleotides, enzyme cofactors with polynucleotides, and combinations and permutations thereof.

The molecular ratio of the recognizing portion on the bridging entity, to the polynucleotides sequence portion thereon need not necessarily be 1:1. There may be many more polynucleotide sequence portions than recognizing portions, or vice versa. In the case when the ratio of polynucleotide sequence portion to recognizing portion on the bridging entity is greater than 1, for example, 5, 10 or greater, the system amplifies the primary recognition event by a factor equal to the ratio.

Among preferred bridging entities of the invention are circular polymers of single- or double-stranded DNA. The single-stranded ones include so-called filamentous phages, such as fd, f1 and M13 (see Van Wezenbeek, P., Gene, 11: 129 (1980).) These filamentous phages do not lyse their host; rather, they are released from infected cells as the cells continue to grow and divide. M13 is commercially available (Bethesda Research Labs, Inc.) and has been extensively used as a cloning and sequencing system. It can be cut at a restriction endonuclease site to incorporate therein any desired polynucleotide probe sequence, to serve as the recognizing portion of the bridging entity. Either at the same site or at a different site, the circular DNA can be opened to incorporate the polynucleotide portion of the bridging entity, capable of annealing to the complementary portion on the signalling entity. In this manner, a bridging entity is obtained which is capable or recognizing a gene sequence on an analyte by hybridization, and is also capable of annealing to the signalling entity through another sequence thereon. (A generalized system of this sort is shown in FIGURE 2.)

In one particularly preferred embodiment, the bridging entity comprises a DNA polymer which carries the sequence for a given gene (for example, a viral probe such as hepatitis B virus, EBV and the like), and, at another place in the polymer, a poly G, or poly GT, or poly dG, or poly dC, or poly dCA, or poly dGdT polynucleotide portion. Ideally, a single-stranded DNA polymer can be provided carrying the polynucleotide portion capable of annealing to the signalling entity (e.g., poly dGT), and also carrying a restriction endonuclease site, so that the user can incorporate any desired DNA probe thereinto. In this manner, by a few simple enzymatic manipulations, the DNA polymer bridging entity can be quickly transformed into a wide variety of bridging entities.

The signalling entity of the invention needs to carry both a polynucleotide portion capable of annealing to the complementary portion on the bridging entity, and a signal generating portion.

The polynucleotide portion on the signalling entity is defined by the same parameters as the complementary portion on the molecular bridging entity. It should be of a length capable of forming stable polynucleotide hybrids with the corresponding polynucleotide on the bridging entity. "Annealing" as used in this part of the invention refers to the required base pair matching between two complementary polynucleotide strands, under any given set of stringency conditions. It is generally understood in the art that about 12 to 13 nucleotides in a row are necessary for stable annealing. Thus, as a minimum, the number of nucleotides in the sequence should be that necessary for stable annealing with the polynucleotide portion of the bridging entity. The formation of the hybrid should be stable enough to withstand any washing, elution, or signal detection procedures which follow hybridization.

The "signal generating" portion of the signalling entity can encompass virtually any of the signal generating systems used in the prior art, and any system to be developed in the future. It comprises a moiety which generates a signal itself (e.g., a radiolabel), or a moiety which, upon further reaction or manipulation will give rise to a signal (e.g., an enzyme-linked system). Both types are herein called "signal generating" portions.

Thus, the signal generating portion may comprise a radiolabel (e.g., ^{14}C, ^{32}P, ^{3}H, and the like), an enzyme (e.g., peroxidase, alkaline or acid phospha-

tase, and the like), a bacterial label, a fluorescent label, an antibody (which may be used in a double antibody system), an antigen (to be used with a labeled antibody), a small molecule such as biotin (to be used with an avidin, streptavidin, or antibiotin system), a latex particle (to be used in a buoyancy or latex agglutination system), an electron dense compound such as ferritin (to be used with electron microscopy), or any combinations or permutations thereof.

For example, if the signal generating portion of the signalling entity is an antigen, a signal can be generated by complexing said antigen with an antibody/enzyme conjugate, followed by addition of enzyme substrate. If the signal generating portion of the signalling entity were an antibody, signal can be generated by complexing anti-antibody or an F_c binding protein such as Protein A therewith, which second antibody or Protein A have been conjugated to an enzyme.

Among the preferred signal generating portions are those based on the biotin/avidin system. This system can be incorporated into the signalling entity by a variety of means. For example, the polynucleotide portion of the signalling entity can be covalently attached to biotin via a cytochrome c bridge (Manning et al, Biochemistry, 16: 1364-1370 (1977), Manning et al, Chromosoma, 53: 107-117 (1975), Sodja, A., Nucleic Acids Research, 5: 385-401 (1978)), or the biotin can be covalently incorporated into specific nucleotide residues (Langer, P.R., Proceedings of the National Academy of Sciences, USA, 78: 6633-6637 (1981)), or the biotin can be attached to a polynucleotide by means of a diamine (e.g., pentane diamine) bridge (Broker, T.R., et al, Nucleic Acids Research 5: 363-384 (1978)). Interaction of the biotin molecules in the signal generating portion with avidin, streptavidin or antibiotin antibodies is then carried out, wherein the avidin, streptavidin or the antibodies are conjugated to such signalling components as latex particles (Sodja, A., et al, supra, or Manning, et al Chromosoma, supra), ferritin (Broker, supra), a fluorogen such as fluorescein, an enzyme, or the like,

A thorough description of various non-radioactive signal generating systems, both biotin/avidin-based and non-biotin/avidin-based can be found in two presently copending patent applications: Publication Number 82-301804.9 filed at the European Patent Office on April 6, 1982 to "Modified Nucleotides and Methods of Preparing and Using Same" by Ward et all (EP-A-63879), and Publication Number 83-106112.2, filed on June 22, 1983 at the European Patent Office to "Modified Nucleotides, Methods of Preparing and Utilizing, and Compositions Containing the Same" by Engelhardt et al (EP-A-97373).

In addition, the signal generating portion of the signalling entity need not be a polynucleotide which has been chemically modified or artificially altered in any way. Some biological systems perform in vivo modifications which can be utilized by this sytem. One such system is the phage T_4 grown in E. coli. T_4 DNA has a very high content of glycosylated C residues. It is possible to insert (clone) a low complexity repeating polynucleotide sequence into phage T_4. This phage would then be naturally propagated and glycosylated in the host. The viral DNA can be isolated from E. coli and bound to a complementary sequence on the bridging moiety. Detection could then be accomplished via a lectin/enzyme system, or lectin/fluorescent dye, or lectin/electron dense material, or lectin/radioactive label, using the natural glucose residues on the T_4 DNA as points of anchorage. Other T (even) phages such as T_2, T_6, or T_8 can also be used.

The number of signal generating portions need not have a 1:1 stoichiometry with the number of polynucleotide portions on the signalling entity. When the ratio of signal generating portions to polynucleotide portion in the signalling portion of the signalling entity is greater than 1 (e.g. greater than 5, or greater than 10), the system functions as an amplification system. Thus, for example, if there are 10 signal generating portions per polynucleotide portion in the signalling entity, a 10:1 signal amplification over the bridging entity is obtained. If, in addition, the bridging entity has a signal amplification system itself, i.e., the ratio of polynucleotide portions to recognizing portions on the bridging entity is greater than 1, the overall signal amplification system is the product of both ratios. This means that for every primary recognition event occurring at the level of analyte, the amplification quickly increases and leads to very sensitive systems. This factor can be readily controlled by the design of the system components.

PROCESSES OF PREPARATION

The bridging entity, as stated previously, needs to comprise a recognizing portion and a polynucleotide portion. The signalling entity requires a polynucleotide portion and a signal generating portion. Thus, generally, the method of preparation of individual components in the system will relate to the covalent attachment of polynucleotides, or individual components thereof, to 1) protein moieties, 2) saccharide moieties, 3) other polynucleotide moieties, 4) small molecular weight compounds (e.g., MW less than about 1000), 5) radiolabels, or 6) insoluble phases such as bacterial particles, or latex particles. Therefore, the chemistry involved in the covalent attachment or conjugation of nucleic acids to their corresponding partner or partners is well within the skill of the art.

The covalent attachment of polynucleotide sequences to proteins is well described in the literature. Normally, the reaction is carried out directly by carbodiimid crosslinking (Halloran, M.K. J. Immunol. 373

(1966) or by cross-linking the protein to the nucleic acid in th presenc of such agents as formaldehyde (s e .g., Brutlag, D. et al, Biochemistry, 8: 3214-3218 (1969), Manning, J.E., et al, Chromosoma, 53: 107-117 (1975)), (4-azidophenyl) glyoxal (Politz, S.M., Biochemistry, 20: 372-378 (1981)); by oxidation of 2',3'-hydroxy ends of a polyribonucleotide, followed by i) Schiff base formation with the amine groups of a protein, and by ii) borohydride reduction (Sodja, A., et al, Nucleic Acids Research, 5: 385-401 (1978)). Other methods include direct bromination of DNA (Jones, A.S., Nature 183: 1603 (1959) followed by reaction with diaminohexane (Lowe, C.R., Eur. J. Biochem. 73: 265-274, (1977)), and coupling via protein carboxyl functions; or by mercuration of cytosine moieties (Dale, R.M.K. et al, P.N.A.S., 70: 2236-2242, (1973)) followed by halogenation (Dale, R.M.K. et al, Nucleic Acids Res. 2:915-930 (1975)), reaction with diaminohexane and coupling to protein carboxyl groups.

Of particular interest is the use of dicarbonyl reagents for chemical modification of guanine bases in the preparation of the signalling entity. This represents one of the particularly useful advantages of the present multi-component assay system. If the polynucleotide portion on the signalling entity has very low G content, it is possible to chemically react said polynucleotide portion with any material via a cross-linking agent such as a dicarbonyl compound, without fear of irreversibly modifying the annealing properties of the polynucleotide portion in question. This applies equally well to the attachment of any small molecular weight molecule to the polynucleotide portion, which attachment depends on the use of dicarbonyl compounds, or other nondiscriminating cross-linking agents. This technique saves the effort and time involved in previously modifying individual nucleotide residues, and then incorporating these into a polynucleotide strand by enzymatic polymerization.

The attachment of polynucleotide sequences to saccharides can be carried out according to Cramer et al, Chem. Ber 92: 384-391 (1959). Saccharides having up to 20 saccharide units are preferred.

The attachment of polynucleotide sequences to other polynucleotide sequences is carried out by either chemical or enzymatic techniques, such as using blunt end ligation or ligation based on the presence of cohesive terminii generated by endonuclease digestion enzymes. The cleavage and ligation of DNA sequences to each other is well described in Helling and Lomax, "The Molecular Cloning of Genes-General Procedures" which is Chapter 1 of "Genetic Engineering" by Chakrabarty, CRC Press, 1978, pages 1-30.

Other methods for attaching polynucleotides to polynucleotides include using SS Dna + Ribo dUTP + Terminal Transferas (Roychoudery, R. + Wu, R., in Meth. in Enz., LXV, 43, (1980)); Periodate oxidation, reductive amination with amino derivatives including 1,6 diamino hexane (1), 3-aminopropionic acid (2), or bis (2-amino ethanethiol) (3), (Perikeh, I Mach, S. and Cuatrecasas, in Meth. in Enz. XXXIV, 82 (1974)); or by limited bromination of C (through mercuration) (Dale & Ward supra) and subsequent reaction of DNA with same reagents ((1), (2) + (3)).

DNA derivatives of compounds (1) or (2), above, can subsequently be coupled to proteins via water-soluble carbodiimide derivatives (Inman, J.K. in Meth in Enz., XXXIV, 52-53) (1974). In case (3), the protein can be activated with the N-hydroxy succinimide ster of bromoacetic acid. The resulting activated protein can be covalently linked to the thiolated nucl ic acid at room temperature.

The covalent incorporation of radiolabels such as ^{32}P into DNA sequences can be done by any of a variety of methods, such as direct incorporation of radiolabeled nucleotides by enzymatic polymerization, nick translation, and the like (Rigby et al, J. Mol. Biol. 113: 237-251 (1977).)

The preparation of the individual elements of th signal generating system such as protein/latex conjugates, protein/ferritin conjugates, antibody/enzym conjugates, fluorogen/antibody conjugates, avidin/enzyme conjugates, and the like is generally well known in the art and will be not described in further detail.

The specific preparation of individual polynucleotide sequences is also well understood by those of skill in the art. For example, if a polynucleotid s - quence comprises a gene or genes, the same can b prepared by synthetic procedures, or can be prepared by reverse transcription of mRNA using reverse transcriptase to generate a complementary DNA. If the polynucleotide sequence comprises a strand of any one nucleotide (e.g., poly dG or poly dC) or a strand of any dinucleotide pair (e.g., poly dGT, or the like), the same can be readily prepared by enzymatic-based reactions such as by using DNA polymerase, or by synthetic methodology.

METHODS OF USE

The analyte being detected can be present in any biological or non-biological sample, such as clinical samples, for example, blood, urine, feces, saliva, pus, semen, serum, other tissues, fermentation broths, culture media, and the like.

If necessary, the analyte is preextracted or purified by methods known to concentrate the particular type of analyte from its admixing components. For example, if the analyte is a protein or protein-containing fraction, protein extraction procedures such as salt precipitations, alcohol precipitations or chromatography can be utilized. If the analyte comprises a nucl ic acid s gment to be identified, nucleic acid extraction procedures, such as phenol extraction, can be utiliz d. Th analyte, together with impurifying

materials if such be the case, can be tested in the mixture as purified or, especially when it is a nucleic acid segment, can be immobilized (see for example, Wahl et al U.S. Patent 4,302,204.)

The composition suspected of containing the analyte is incubated with the bridging entity for a time and under conditions sufficient to allow complexation between the recognizable portion of the analyte and the recognizing portion on the bridging entity. These conditions will vary depending on the nature and amount of the analyte and of the bridging entity. Normally, after complexation has occurred, the sample is washed with neutral solution to remove excess bridging entity. Alternatively, no wash is carried out at this stage but signalling entity is added to the mixture and a wash is carried out after annealing has occurred between the polynucleotide strands on the bridging entity and on the signalling entity respectively. Hybridization of the bridging entity strand to the signalling entity strand is carried out under hybridizing conditions and under any set of stringency conditions. A final wash may be necessary prior to generation of signal.

Signal generation is carried out by any given technique, depending on the nature of the signal generating system. Thus, if an enzyme linked assay is utilized, the ternary complex between analyte, bridging entity and signalling entity is allowed to incubate with the enzyme carrying reagent (e.g., enzyme/antibody conjugate), and substrate is added thereto to develop color. Alternatively, enzyme might be attached directly to the polynucleotide strand on the signalling entity, in which case substrate is added immediately thereafter to obtain color development. If the signal generating portion of the signalling entity is a biotin moiety, then a biotin reactive molecule such as avidin, streptavidin or anti-biotin antibody, is added thereto. The biotin reactive molecule is conjugated to an enzyme, a fluorescent compound, an electron dense compound, or an insoluble solid phase, and detection is carried out by appropriate means.

APPLICATIONS

The applications of the system of the invention are unlimited. Any analyte desired to be detected and analyzed in any sample can be subject to the method of the invention.

For example, the system can be used for microorganism detection and identification, by using any of a variety of recognizable portions and recognizing portions in the analyte and the bridging entity respectively.

Of particular interest is the detection and identification of viral and bacterial DNA sequences.

The method can be utilized to diagnose genetic disorders by preparing a polynucleotide complementary to a DNA gene sequence which is associated with the genetic disorder, and detecting the presence of any primary recognition events. Among these genetic diseases, for example, can be mentioned thalassemia. The determination of thalassemia can be made (for known genetic defects) by hybridization of oligonucleotides to genomic DNA followed by specific washing procedures or by restriction analysis and Southern, Northern, or Dot blots.

Another use for the system of the invention is in chromosomal karyotyping, which comprises using a series of modified polynucleotides corresponding to a series of defined genetic sequences located on chromosomes, and then detecting primary recognition events thereon.

Another use includes a method for identifying or locating hormone receptor sites on the surface of cells, which comprises binding a hormone receptor binding compound present in the bridging entity to the receptor site, and then detecting primary recognition events by means of the signalling system of the invention.

Another use comprises the detection of cancer, by detecting in the blood or serum of suspect subjects, the presence of cancer associated antigens such as CEA (carcinoembryonic antigen). Another use includes a method of tumor or cancer cell identification or detection which comprises identifying malignant cells by detecting the absence of normal receptors sites by the technique of the invention.

Another use includes a method of detecting antibodies against certain infectious diseases in animals, by using antigen therefor as a recognizing portion in the molecular bridging entity. Sugar levels or differential glycosylated hemoglobin levels can be detected in diabetes by using a lectin as the recognizing portion on the molecular bridging entity.

Yet another use for the process and system of the invention is in the insolubilization of analytes. Thus, if a sample is suspected of containing an analyte, and one wishes to extract and purify the analyte from the sample, the "signalling entity" is designed so that the signal generating portion comprises or is capable of specifically binding to an insoluble solid phase, such as a natural or synthetic aqueous insoluble resin, a glass, a plastic such as an acrylate or methacrylate, the inside of a test tube wall, or of a well, and the like. The bridging entity is allowed to incubate with the solid phase, thus creating recognition sites (i.e., affinity surfaces) for the analyte, which is then bound thereto.

The present invention lends itself readily to the preparation of kits comprising one or more of the elements necessary to perform the detection and identification process. Thus, a kit may comprise a carrier being compartmentalized to receive in close confinement therein one or more container means or series of container means such as test tubes, vials, flasks, bottles, syringes, or the like. A first of said container means or series of container means may contain th

bridging entity, for recognition of any of a wide variety of analytes. A second container means or series of container means may contain signalling entities. A third container means or series of container means may contain predetermined amounts of analyte, so as to provide the ability to construct a standard curve into which results can be interpolated. Other container means or series of container means may contain the elements necessary to generate the signal, such as enzyme linked conjugates, avidin linked conjugates, ferritin linked conjugates, latex linked conjugates, fluorogen linked conjugates, and the like.

In a preferred embodiment, the kit carrier contains a first container means comprising a bridging system which is DNA carrying a polynucleotide portion of predetermined sequence and a restriction site or cleavage site on the DNA which can be used to incorporate any of a number of gene probes for testing and identifying genetic sequences associated with the analyte. Another container means in this preferred kit would comprise a signalling entity carrying a polynucleotide portion complementary to the polynucleotide portion present in the DNA present in the first container means, and a signal generating portion which may be any of the aforementioned systems. A third container means or series of container means in this preferred kit may comprise a variety of DNA probes complementary to the genetic sequences present on one or more polynucleotide-containing analytes such as viruses, bacteria, cells and the like.

Thus, the user would utilize a cleavage method (such as use of a restriction endonuclease) to open the DNA in the first container, incorporate thereinto any desired DNA probe present in the third container or container series, ligate the polymer and then utilize the bridging entity and the signalling entity to detect and identify the presence of any desired genetic sequence present in the analyte. It should be kept in mind that a single strand cannot be cut with a restriction enzyme unless a linker (which spans the site) is first hybridized to it, thereby creating a double-strand in that location. Normally the gene would be ligated into the RF (double-stranded) so that it could be amplified in a microorganism. Preferred embodiments of the present invention are explained in detail in the following enumeration:

1. A method of detecting in a sample an analyte (A) having a molecularly recognizable portion thereon, which comprises:

providing a molecular bridging entity (B) having thereon:

(i) a portion capable of recognizing said molecularly recognizable portion on said analyte; and

(ii) a portion comprising a polynucleotide sequence; and

(C) a signalling entity having thereon:

(i) a polynucleotide portion capable of annealing to said polynucleotide portion of said bridging entity, thereby to form a stable polynucleotide hybrid, and

(ii) a signal generating portion;

forming a complex comprising:

(1) said analyte (A) complexed through said molecularly recognizable portion to

(2) said recognizing portion of said entity (B); said entity (B) being complexed through said polynucleotide portion thereon to

(3) said polynucleotide portion of said signalling entity (C), with the proviso that when said analyte is a polynucleotide, the signal generating portion is not an enzyme that is covalently linked to said recognition portion and

detecting a signal by means of said signal generating portion present in said complex.

2. The method of item 1 wherein said analyte is present in a biological or non-biological sample.

3. The method of item 1 wherein said molecularly recognizable portion on said analyte is proteinaceous.

4. The method of item 1 wherein the molecularly recognizable portion on said analyte comprises nucleic acid.

5. The method of item 1 wherein the molecularly recognizable portion on said analyte comprises a saccharide.

6. The method of any of items 3, 4 or 5 wherein said analyte is selected from the group consisting of an antigen, an antibody, a receptor, a virus, a viral component, a bacterium, a bacterial component, a cell, a cellular component, or any pathogenic or non-pathogenic component of a sample.

7. The method of item 1 wherein said recognizing portion on said bridging entity comprises a polynucleotide sequence.

8. The method of item 1 wherein said recognizing portion on said bridging entity comprises an antigen.

9. The method of item 1 wherein said recognizing portion on said bridging entity comprises an antibody.

10. The method of item 1 wherein said recognizing portion on said bridging entity comprises a saccharide.

11. The method of item 1 wherein said recognizing portion on said bridging entity comprises a lectin.

12. The method of item 1 wherein said recognizing portion on said bridging entity comprises a hormone.

13. The method of item 1 wherein said recognizing portion on said bridging entity comprises a receptor.

14. The method of item. 1 wherein said recognizing portion on said bridging entity comprises an enzyme inhibitor or enzyme cofactor.

15. The method of item 1 wh rein said r cognizing portion on said bridging ntity compris s an enzym active site, a c factor binding site, or a receptor protein.

16. The method of item 1 wherein said polynucleotide sequence on said bridging entity codes for a gene product or fragment thereof.

17. The method of item 1 wherein said polynucleotide sequence on said bridging entity does not code for a gene sequence or fragment thereof.

18. The method of item 1 wherein said polynucleotide sequence on said bridging entity comprises a poly deoxy G, poly deoxy C, poly deoxy T or poly deoxy A sequence, or any poly-ribo or -deoxyribo purine, pyrimidine or analog.

19. The method of item 1 wherein said polynucleotide sequence on said bridging entity comprises a sequence portion which is rich in guanosine residues.

20. The method of item 1 wherein said polynucleotide sequence in said bridging entity is covalently attached to another polynucleotide sequence.

21. The method of item 1 wherein said polynucleotide sequence in said bridging entity is covalently attached to an antibody.

22. The method of item 1 wherein said polynucleotide sequence in said bridging entity is covalently attached to an antigen.

23. The method of item 1 wherein said polynucleotide sequence in said bridging entity is covalently attached to a saccharide.

24. The method of item 1 wherein said polynucleotide sequence in said bridging entity is covalently attached to a lectin.

25. The method of item 1 wherein said polynucleotide sequence in said bridging entity is covalently attached to a hormone.

26. The method of item 1 wherein said polynucleotide sequence in said bridging entity is covalently attached to a receptor.

27. The method of item 1 wherein said polynucleotide sequence in said bridging entity is covalently attached to an enzyme inhibitor or enzyme cofactor.

28. The method of item 1 wherein said polynucleotide sequence in said bridging entity is covalently attached to an enzyme.

29. The method of item 7 wherein said bridging entity is a circular DNA polymer.

30. The method of item 29 wherein said DNA is single-stranded.

31. Th method of it m 29 wherein said circular DNA polym r is deriv d from a filamentous phage.

32. The m thod of item 31 wh rein said filamentous phage is M13 or a variant thereof.

33. Th m thod of it m 32 wher in said M13 phage carri s a sequenc portion which is rich in guanosin r sidues, or cytosine residues.

34. Th method of item 1 wherein said polynucl otide portion on said signalling entity codes for a gene product or fragment thereof.

35. The method of item 1 wherein said polynucleotide portion on said signalling entity does not code for a gene product or fragment thereof.

36. The method of item 1 wherein said polynucleotide portion on said signalling entity comprises a poly deoxy C, poly deoxy G, poly deoxy A, poly deoxy T sequence, or a repeating sequence of low complexity.

37. The method of item 1 wherein said polynucleotide portion on said signalling entity comprises a sequence portion which is rich in cytosine residues, or guanosine residues.

38. The method of item 1 wherein said signalling entity is a polynucleotide polymer.

39. The method of item 38 wherein said polynucleotide polymer is a naturally occurring modifi d DNA.

40. The method item 39, wherein said polynucleotide polymer is derived from a T (even) phage.

41. The method of item 40 wherein said T (ev n) phage phage is T_4.

42. The method of item 39 wherein said modified DNA carries a cloned insert.

43. The method of item 38 wherein said polym r is single-stranded.

44. The method of item 43, wherein said polymer is derived from a filamentous phage.

45. The method of item 44 wherein said phage is M13 or a variant thereof.

46. The method of item 1 wherein said signal g nerating portion of said signalling entity is radiolabeled.

47. The method of item 1 wherein said signal generating portion of said signalling entity is not radiolabeled.

48. The method of item 47 wherein said signal generating portion comprises an enzyme.

49. The method of item 47 wherein said signal generating portion comprises a biotin moiety.

50. The method of item 47 wherein said signal generating portion comprises a fluorogenic compound.

51. The method of item 47 wherein said signal generating portion comprises an electron dense compound.

52. The method of item 47 wherein said signal generating portion comprises or binds to an insoluble phase.

53. Th method of item 52 wher in said insoluble phase compris s a latex particl , a resin, or a bacterium.

54. The method of it m 47 wher in said signal

g neration portion compris s an antibody or antigen.

55. The method of item 47 wherein said signal generating portion comprises a saccharide or lectin.

56. The method of item 1 wherein said step of detecting a signal by means of said signal generating portion comprises a radioactivity measurement.

57. The method of item 1 wherein said step of detecting a signal by means of said signal generating portion comprises an enzymatic reaction.

58. The method of item 1 wherein said step of detecting a signal by means of said signal generating portion comprises a fluorescence measurement, or electron microscopic measurement.

59. The method of item 47 wherein said signal generating portion is a polynucleotide sequence capable of recognizing a signal containing moiety.

60. The method of item 1 wherein said step of detecting a signal by means of said signal generating portion comprises an antibody/antigen complexation reaction.

61. The method of item 1 wherein said step of detecting a signal by means of said signal generating portion comprises a complexation reaction between biotin and a biotin binding moiety.

62. The method of item 61 wherein said moiety is avidin, streptavidin or an anti-biotin antibody.

63. The method of item 1 wherein said step of detecting a signal by means of said signal generating portion comprises detection of an electron dense compound.

64. The method of item 1 wherein said step of detecting a signal by means of said signal generating portion comprises a complexation reaction between a saccharide and a lectin.

65. The method of item 1 wherein said step of detecting a signal by means of said signal generating portion comprises a binding step on an insoluble phase.

66. The method of item 1 wherein said step of detecting a signal by means of said signal generating portion comprises complexation between a signalling entity comprising a cloned insert on a naturally-occurring modified DNA, and the bridging moiety, followed by binding a modified lectin to said signalling entity.

67. The method of item 66 wherein said modified DNA is derived from a T_4 phage.

68. The method of item 65 wherein said insoluble phase is a latex particl .

69. Th method of it m 1 wher in said recognizable portion on said analyt is a polynucleotid sequence, said r cognizing portion on said bridging entity is a polynucl otid sequ nc capabl of stably annealing th reto, said bridging entity is a single-strand d DNA polymer, and said step of det ction by means of said signal generating portion on said signalling ntity is based on non-radioactiv detection.

70. Th method of it m 69 wherein said bridging entity is derived from a filamentous phage.

71. The method of item 69 wherein said signalling entity is derived from a filamentous phage.

72. A polynucleotide sequence covalently attached to an antibody.

73. The sequence of item 72 wherein said antibody is monoclonal.

74. A polynucleotide sequence covalently attached to a lectin.

75. A polynucleotide sequence covalently attached to a saccharide having up to 20 saccharide units.

76. A polynucleotide sequence covalently attached to receptor.

77. A polynucleotide-sequence covalently attached to a hormone.

78. A DNA molecule carrying a polynucleotide portion which comprises a sequence selected from the group consisting of poly dGT, poly dAC, poly dCT, poly dAt, poly dGC, poly dGA, poly dG, poly dC, poly dT, poly dA, and a repeating low-complexity polynucleotide.

79. The DNA molecule of item 78 which is a filamentous phage.

80. The phage of item 79 which is M13 or a variant thereof.

81. The DNA molecule of any of items 78 or 79 wherein said sequence is at least an oligonucleotide.

82. The DNA molecule of any of items 78 or 79 which also carries a polynucleotide sequ nce complementary to part of whole of a gen sequence of a nucleic acid-containing organism.

83. The DNA molecule of item 82 wherein said organism is a virus, a prokaryotic or a eukaryotic cell.

84. The DNA molecule of item 83 wherein said prokaryotic cell is a bacterium.

85. The DNA molecule of item 83 wherein said eukaryotic cell is a mammalian cell.

86. The DNA molecule of item 82 which is a filamentous phage.

87. The DNA molecule of item 82 which is M13 or a variant thereof.

88. A circular DNA molecule covalently attached to a non radiolabelled signal generating moiety.

89. The DNA molecule of item 88 which is a filamentous phag .

90. The DNA mol cule of any of items 88 or 89 which carries a polynucleotide portion which comprises a sequence selected from th group consisting of poly dGT, poly dAC, poly dCT, poly dAT, poly dGC, poly dGA, poly dG, poly dC, poly

dT, poly dA and a repeating low-complexity polynucleotide.

91. The DNA molecule of any of items 88 or 89 which carries a polynucleotide portion which is rich in cytosine residues.

92. The DNA molecule of item 90 wherein said sequence is an oligonucleotide.

93. The DNA molecule of any of items 88 or 89 which carries a polynucleotide portion which comprises a sequence coding for part or whole of a gene.

94. The DNA molecule of any of items 88 or 89 wherein said signal generating moiety comprises a radiolabel.

95. The DNA molecule of any of items 88 or 89 wherein said signal generating moiety is non-radiolabeled.

96. The DNA molecule of item 93 wherein said signal generating moiety comprises an enzyme.

97. The DNA molecule of item 93 wherein said signal generating moiety comprises a biotin moiety.

98. The DNA molecule of item 93 wherein said signal generating moeity comprises an antibody.

99. The DNA molecule of item 93 wherein said signal generating moeity comprises a fluorogenic compound.

100. A kit useful for the detection of an analyte (A) having a molecularly recognizable portion thereon, comprising:

I) a carrier being compartmentalized to receive in close confinement therein one or more container means;

II) a first container means containing a molecular bridging entity (B) having thereon:

(i) a portion capable of recognizing said molecularly recognizble portion on said analyte (A); and

(ii) a portion comprising a polynucleotide sequence; and

(III) a second container means containing a signalling entity (C) having thereon:

(i) a polynucleotide portion capable of annealing to said polynucleotide portion of said bridging entity (B) thereby to form a stable polynucleotide hybrid; and

(ii) a signal generating portion.

101. The kit of item 100 which also comprises

IV) a third container means containing components needed to detect a signal from said signal generating means.

102. The kit of item. 100 wherein said recognizing portion on said bridging entity comprises a polynucl otid s qu nce.

103. The kit of it m 100 wherein said recognizing portion on said bridging entity comprises an antig n.

104. The kit of item 100 wherein said recognizing portion on said bridging entity compris s an antibody.

105. The kit of item 100 wherein said recognizing portion on said bridging entity comprises a saccharid .

106. The kit of item 100 wherein said recognizing portion on said bridging entity comprises a lectin.

107. The kit of item 100 wherein said recognizing portion on said bridging entity comprises a hormone.

108. The kit of item 100 wherein said recognizing portion on said bridging entity comprises a receptor.

109. The kit of item 100 wherein said recognizing portion on said bridging entity comprises an anzyme inhibitor or enzyme cofactor.

110. The kit of item 100 wherein said recognizing portion on said bridging entity comprises an enzyme active site or cofactor binding site.

111. The kit of item 100 wherein wherein said polynucleotide sequence on said bridging entity codes for a gene product or fragment thereof.

112. The kit of item 100 wherein said polynucl otide sequence on said bridging entity does not code for a gene product or fragment thereof.

113. The kit of item 100 wherein said polynucleotide sequence on said bridging entity compris s a poly dG, poly dC, poly dT, poly dA sequence, or a low complexity (repeating) polynucleotide.

114. The kit of item 100 wherein said polynucl otide sequence on said bridging entity comprises a sequence portion which is rich in guanosin residues.

115. The kit of item 100 wherein said polynucleotide sequence in said bridging entity is covalently attached to another polynucleotide sequence.

116. The kit of item 100 wherein said polynucl otide sequence in said bridging entity is covalently attached to an antibody.

117. The kit of item 100 wherein said polynucleotide sequence in said bridging entity is covalently attached to an antigen.

118. The kit of item 100 wherein said polynucl otide sequence in said bridging entity is covalently attached to a saccharide.

119. The kit of item 100 wherein said polynucleotide sequence in said bridging entity is covalently attached to a lectin.

120. The kit of item 100 wherein said polynucleotide sequence in said bridging entity is covalently attached to a hormone.

121. The kit of item 100 wherein said polynucleotid sequence in said bridging entity is covalently attached to a r c ptor.

122. The kit of item 100 wherein said polynucleotide s quence in said bridging entity is coval ntly attached to an enzym inhibitor or enzyme cofactor.

123. The kit of item 100 wherein said polynucl otid sequenc in said bridging entity is covalently attached to an enzyme.
124. Th kit of item 100 wherein said bridging entity is a circular DNA polymer.
125. The kit of item 124 wherein said circular DNA is single-stranded.
126. The kit of item 125 wherein said circular DNA polymer is derived from a filamentous phage.
127. The kit of item 124 wherein said filamentous phage is M13 or a variant thereof.
128. The kit of item 125 wherein said M13 phage carries a sequence portion which is rich in guanosine or cytosine residues.
129. The kit of item 100 wherein said polynucleotide portion on said signalling entity codes for a gene product or fragment thereof.
130. The kit of item 100 wherein said polynucleotide portion on said signalling entity does not code for a gene product or fragment thereof.
131. The kit of item 100 wherein said polynucleotide portion on said signalling entity comprises a poly dC, poly dG, poly dA, poly dT sequence, or a low-complexity, repeating polynucleotide.
132. The kit of item 100 wherein said polynucleotide portion on said signalling entity comprises a sequence portion which is rich in cytosinee or guanosine residues.
133. The kit of item 100 wherein said signalling entity is a circular DNA polymer.
134. The kit of item 133 wherein said DNA is single-stranded.
135. The kit of item 134 wherein said DNA is derived from a filamentous phage.
136. The kit of item 135 wherein said phage is M13 or a variant thereof.
137. The kit of item 100 wherein said signal generating portion on said signalling entity is radiolabeled.
138. The kit of item 100 wherein said signal generating portion of said signalling entity is not radiolabeled.
139. The kit of item 138 wherein said signal generating portion comprises an enzyme.
140. The kit of item 138 wherein said signal generating portion comprises a biotin moiety.
141. The kit of item 138 wherein said signal generating portion comprises a fluorogen.
142. The kit of item 138 wherein said signal generating portion comprises an electron dense compound.
143. The kit of item 138 wherein said signal generating portion comprises or binds to an insoluble phas .
144. The kit of item 138 wherein said insoluble phase comprises a latex particle, a resin, or a bacterium.
145. The kit of item 138 wherein said signal generating portion compris s an antibody.
146. The kit of item 138 wh rein said signal g nerating portion comprises a saccharide.
147. The kit of item 100 wherein said recognizable portion on said analyte is a polynucleotide sequence, said recognizing portion on said bridging entity is a polynucleotide sequence capable of stably annealing thereto, said bridging entity is a single-stranded DNA polymer, and said signal generating portion on said signalling entity is based on non-radioactive detection.
148. The kit of item 147 wherein said bridging entity is derived from a filamentous phage.
149. The kit of item 147 wherein said signalling entity is derived from a filamentous phag .

Especially preferred. embodiments of the invention are the following:

150. A method of detecting in a sample an analyte (A) having a molecularly recognizable portion thereon, which comprises:

providing a molecular bridging entity (B) having thereon:

(i) a portion capable of recognizing said molecularly recognizable portion on said analyte (A), and

(ii) a portion comprising a recognizable modifier, and

a signalling entity (C) having thereon:

(i) a receptor for said recognizable modifier capable of attachment or binding to said r cognizable modifier of said bridging entity (B) thereby to form a stable complex, and

(ii) a signal generating portion, and

forming a complex comprising:

(1) said analyte (A) attached through said molecularly recognizable portion thereon to

(2) said portion of said molecular bridging ntity (B) capable of recognizing said mol cularly recognizable portion of analyte (A), said molecular bridging entity (B) being compl xed via said recognizable modifier thereon to

(3) said signalling entity (C) via said receptor thereon capable of attachment to or binding to said recognizable modifier said bridging entity (B).

151. A stable detectable complex comprising a target analyte, a modified first receptor attached thereto via said receptor portion, the modifying portion thereof being attached to a second receptor for said modifying portion of said first receptor, said second receptor having attached thereto a signalling entity.

152. An ntity capable of detecting a protein r ceptor comprising:

(a) a protein capable of binding said protein receptor,and

(b) a polynucleotide attached to said prot in that is capable of binding said protein recep-

tor.

153. The entity of it m 152 which further comprises a signal g nerating portion attached to said polynucleotide.

Having now generally d scribed this invention, the same will be illustrated by reference to certain specific embodiments which are included herein for purposes of illustration only and are not intended to be limiting unless otherwise specified.

Examples

Examples 1-31 relate to processes of preparation of bridging and signalling moeties. The examples show preparation methods which may be classified within the following categories:

1) Chemical activation of oligonucleotides for subsequent coupling to proteins, saccharides and small molecules.

2) Chemical activation of proteins for subsequent coupling to DNA, saccharides and small molecules.

3) Chemical activation of saccharides for subsequent coupling to DNA, protein and small molecules.

4) Chemical activation of small molecules for subsequent coupling to DNA and protein.

5) Coupling of DNA to protein, saccharides and small molecules.

The examples classified within the above categories are as follows:

1) Chemical activation of Oligonucleotides.
   A. By terminal ribonucleotide labelling followed by periodic oxidation and reductive amination: Examples 11, 12;
   B. By non-specific bromination: Examples 28, 29, 30.
   C. By specific activation of cytosine moieties via 5-iodocytosine: Examples 16, 17 18.
   D. By specific activation of guanosine moieties via reaction with 3, 4, 5-trichlorodiazobenzene: Example 1.
   E. By specific activation of adenosine and guanosine-moieties via reaction with 2,3-dibromopropanal: Example 9.
2) Chemical Activation of proteins
   A. By bromoacetylation: Examples 13, 14.
3) Activation of saccharides
   A. By activation of reducing saccharides: Examples 4, 5, 6.
   B. By activation of non-reducing saccharides: Examples 7, 8.
4) Activation of small moi ties
   A. Biotin: Exampl s 2, 33, 23, 24, 25, 26
   B. DCTA: Example 3.
5) Coupling of DNA to prot in, saccharides and small molecules
   A. To protein: Exampl s 15, 19, 20.
   B. Saccharid s: Example 19, 18.
   C. To small m lecul s: Exampl s 19, 10, 21, 27.

Exampl 1

Activation of DNA with 3,4,5-Trichloraniline

100 mg of 3,4,5-trichloroaniline were dissolved in 2.5 ml of 0.5M HCl in 50% DMSO and cooled on ice, under vigorous stirring, an equimolar amount of $NaNO_2$ from a cold 1M solution were added, as rapidly as possible, and then stirring was continued for 10 minutes. 1 mg of 3H or fd DNA in 300 µl of water were mixed with 300 µl of 2M cacodylate buffer pH 6.6 and 500 µl DMSO. (By addition of DMSO the pH of the solution rises to 8.3). 20 µl of the freshly prepared diazonium solution were added thereto and the mixture was incubated for two hours at room temperatur . The slight precipitate which appeared during the incubation was removed by centrifugation. The solution was then made 0.4 M with ammonium acetate and the DNA was precipitated with ethanol.

Example 1a

Reaction of Trichloroaniline-activated DNA with thiols. Example of Reaction with DCTA-SH and thiol activated mannose

Fd DNA activated with 3,4,5-Trichloroaniline (Example 1) was dissolved in 0.1M sodium hydroxid with an equal amount of 0.1M K_2HP0_4. This solution was treated with an equal volume of 0.1M DCTA-SH (Example 3) or thiol activated mannose (Ex. 6 and 9), and incubated under argon at 65° for 2 hours. The precipitated disulfides were removed by centrifugation and the DNA was purified by G50 chromatography and stored at -20°C. Using radioactive Ni to level the derivatized DNA, it was determined that 60% of guanines had been labelled.

Example 2

Biotin-SH

Three milimoles of Biotin -NHS ester were dissolved in 25 ml of anhydrous DMF and mixed with a 1M solution of cysteamine hydrochloride in 12 ml of 0.5M sodium bicarbonate and the mixture was incubated at room temperature overnight. During the incubation a heavy precipitate appeared. The liquid was removed under reduced pressur at 45°C and the r - sidue was suspended in 50 ml absolute ethanol, 1 g of $NaBH_4$ was add d and the suspension was stirred for one hour at 75°C. The ethanol was removed and cold 1 M HCl was added to bring the pH to 4.5, and the wat r was removed und r reduced pressure at

35°C. (All thes operations wer performed under an argon atm sphere. to prevent oxidation of the thiol.) The solid residue was p wdered and triturated with 4 ml of cold deareated 0.01 M acetic acid. Thes procedure was rep ated twice and the residu was lyophilized TLC chromatography showed that the main biotin spot contained thiol; two minor spots were thiol negative. In all reactions the amount of biotin used was based on the thiol content.

Example 3

DCTA-SH

One millimole of DCTA-bromide,1,2-diaminocyclohexane-N, N,N,N-tetraacetic acid, was added to 5 ml of 50% DMF containing 0.2 ml of 2,3-dithioethylene and 0.5 ml of triethylamine. The mixture was incubated under argon for 2 hours at 60-70°C. The solution was then mixed with 20 ml of water and loaded onto a Dowex AG-1 column of 9 ml bed volume. The column was washed with 50 ml of 0.1M acetic acid solution until the flowthrough was thiol free. The DCTA-SH was then eluted with 0.25M HCl. The thiol containing fractions were combined, evaporated to dryness under reduced pressure at 40°C and the free acid (300mg) was stored at -20°C under argon.

Example 4

1-0-Methyl-6-0-Tosyl-α-D-mannopyranoside

Non-reducing saccharides were activated through the primary alcohol group by forming the tosylate, and displacing it with ammonia to form an amino group, or with a dithiol to form a thiol group. An example is described here, the activation of α-methyl-d-mannoside, a non-reducing sugar and of mannose as a reducing one. The tosylation was performed analogous to a published procedure (F. Cramer et al. Chem. Ber. 92, 384-391 (1979).)

23 g of methyl-D-mannoside were dissolved in 400 ml of absolute pyridine and the solution was cooled to -15°C on an ice salt mixture. A solution of 24.6 g of p-Toluene sulfonyl chloride in 80 ml absolute pyridine was added to the vigorously stirred mixure and reacted at -15°C for 30 minutes and 12 hours at 20°C. The pyridine was removed under reduced pressure at 40°C and the residue was dissolved in chloroform. The solution was warmed to 50°C and washed successively with 0.5 M potassium hydrogen sulfate followed by 0.5M potassium bicarbonate solution at 50°C (the 50 d gree temperatur was n c ssary to avoid gel formation).

Example 5

6-amino- α -m thyl-D-mannoside hydrochloride

A soluti n of 6 g of th tosylat (Exampl 4) in 130 ml absolute methanol was saturated at 1°C with dry ammonia and autoclaved for 16 hours at 120°C. The dark reaction product was refluxed with charcoal and methanol was removed by distillation leaving a slight yellow syrup. The syrup was dissolved in water and the sulfonate liberated during the displacement reaction was removed by passing the solution through an anion exchanger. HCl was added to the elutate to bring the pH to 5.0 and the water was removed under reduced pressure at 40°C. The residue was triturat d with a mixture of 15 ml of absolute methanol and 15 ml of absolute ether and the solid material was dissolved in 50 ml of absolute methanol and cooled, th addition of 25 ml absolute ether initiated crystallization, yielding 2.5 g hydrochloride.

Example 6

S-(2-mercaptoethyl)-6-thio-α-D-methyl-mannopyranoside

6 g of the sugar tosylate (Example 4) were dissolved in 250 ml of absolute methanol containing 20 ml of a freshly prepared solution of sodium methoxide. To the mixture was added 5 ml of 1.2 ethanedithiol. The mixture was autoclaved at 120°C for 10 hour and the reactions product was treated as abov . Yield 3.1 g.

Example 7

2,3,4,6, Tetraacetyl- α,-D-mannopyranosyl chlorid

This compound was prepared analogously to a published procedure (D. Horton, Organic Synthesis Vol 46 p. 1, Wiley N.Y. 1966). 25 g of dried mannose were added slowly with stirring to 60 ml of acetyl chloride. The vessel was connected to a reflux condenser and the mixture was stirred for 16 hours at room temperature. Chloroform, 300 ml, was added through the condenser and the mixture was poured with vigorous stirring onto 300 g of ice and 100 ml of water. The mixture was transferred to a separatory funnel, and the organic phase was poured as fast as possible into a beaker containing ice and 300 ml of saturated sodium bicarbonate solution. The organic phase was separated and dried with 25 g of anhydrous magnesium sulfate. The drying agent was remov d, washed with dry alcohol free chloroform and the c mbined chloroform solution was conc ntrated to 35 ml at a r duced pressure in a rotatory vaporator. At 50°C ether was added to th solution until slightly turbid and the solution left at room tempera-

ture. Th crystals wer removed by filtration and washed with dry ether. Yield 39 g.

Exampl 8

S-(2-mercaptoethyl)-1-β-D-mannopyranosyl sulfide and S-(2-aminoethyl)-1-β-D-mannopyranosylsulfide

To a solution of 10 g acetochloromannose (Example 7) in 60 ml anhydrous DMF, 4 ml of 1.2 ethanedithiol or 5 g cysteamine hydrochloride and 5 of fine powdered sodium carbonate were added to the suspension which was stirred under argon for 6 hours at 70°C. The carbonate was removed and the liquid was evaporated under reduced pressure at 45°C. The residue was dissolved in absolute methanol and freshly prepared 0.1 M sodium methoxide was added to bring the pH to 8.0 and the mixture was stirred for 5 hours at room temperature. 2 ml of glacial acetic acid were added and the liquid was removed under reduced pressure. The residue was recrystallized from acetic acid. Yield 3.1 g.

Example 9

Activation of DNA with 1,2 dibromopropanal

A solution of acrolein (1.7 g) in ether was cooled on an ice bath and 1.3 ml of bromine were slowly added under stirring while waiting for the color to disappear for the next bromine addition. The ether was partially removed by blowing argon over the solution, resulting in a 2 M solution of the 1,2-dibromopropanal (Example 8). The DNA used for the following operations was in the triethylammonium form to facilitate solution in DMF.

0.5 mg of 3H fd-DNA (linear) (partly tritiated) in 250 µl of water were mixed with 3.0 ml of 0.5 M triethylammonium acetate, pH 4.5 in 70% ethanol and 50 µl of the dibromopropanal solution was added. The mixture was stirred in the dark at 37°C for 40 hours. The reaction was monitored by the appearance of fluorescence. The reaction mixture was evaporated to dryness under reduced pressure, and the DNA dissolved in 0.6 ml water and desalted by G 50 filtration with water as the eluant. The fractions containing radioactivity were combined and the volume was reduced to 0.2 ml.

Example 10

Labelling of the 3,4,5-trichloroaniline DNA with DCTA-SH

0.5 mg of the activated DNA (Example 1) in 0.2 ml of water were mixed with 2.0 ml of 0.5 M triethylammonium ac tate in 90% DMF and 50 mg of DCTA-SH in the triethylammonium form were added. The mixture was stirred in th dark for 4 hours at 50°C. The DMF was remov d under reduced pressure at 45°C and the DNA was desalted by G-50 filtration. The degree of labeling was then det rmined by the us of radioactive Ni63. On the average every 5.3 bases were labelled, by calculation.

Similar procedures were used for the biotination and glycosylation of the activated DNA using the thio derivatives of these substances (Examples 2, 6 and 8).

Chemical labelling of DNA

Rationale

Guanosine couples with certain diazonium salts at the 8 position to give stable colored products (H. Fischer, Z. Physiol. Chem. 60, 696-78, (1909)), and at position 2 to form yellow products which are acid labile (H. Kossel, Z. Physiol. Chem. 340, 210, 1965, E.N. Moudrianakis et al, Biochim. Biophys. Acta 123, 421 (1966)). The guanosine residues in the single stranded nucleic acids can couple with diazonium salts and this reaction has been used to fix single stranded nucleic acids to cellulose (J.C. Alwine et al. Methods in Enzymology Vol. 68. p. 220-242, 1979)). If the coupled diazonium compound contains an active group that can be easily substituted by thiols or amin s, then this constitutes an easy method to attach biotin or other groups to single stranded nucleic acids. 3,4,5-trichlorophenyl diazonium chloride is such a substance which has been used by the inventors to add biotin, 1,2-diaminocyclohexane-N,N,N,N-tetraacetic acid (DCTA), and some sugars to a single stranded DNA.

Another possibility to label single stranded nucleic acids is based on the fact that chloracetaldehyde reacts with adenine at pH 4.5 to form a fluorescent etheno derivative (under mild conditions). J.R. Barrio, et al Biochem. Biophys. Res. Commun. 46, 597-604, 1972), cytidine reacts at pH 3.5 and guanine at pH 6.5. At pH 4.5 guanidine does not react at all (P.D. Sattsangi, et al, J. Org. Chem., 42, 3292-3296, (1977).)

By using 1,2 dibromopropanal in place of chloracetaldehyde it was possible to derivatize DNA with an active primary bromide group, which, under mild r - action conditions, reacts with thiol or amine derivatives, offering another method of labeling DNA. These two methods are base specific.

Example 11

Terminal addition of 5'-uridine monophosphate (UMP) to lin ar 3H fd-DNA with Terminal Transferase and 5'-uridine triphosphate.

The incubation mixture of 600 µl contained: 400 µg of DNA, 1mM $CoCl_2$, 0.2 mM dithiothreitol, 0.1 M

cacodylic acid, 25 mM tris bas , 1 mM UTP and 400 units of terminal transferas . Th final pH of the mixture was 6.9-7.0.

The mixture was incubated for 2 hours at 35°C. The DNA was precipitated with ethanol and dissolved in 400 µl 0.2 M sodium acetate pH 4.7.

Example 12

Oxidation of the Terminal Ribo Group and Reductive Amination. Synthesis of Amino, carboxy and thio-end substituted DNA.

The incubation mixture of 450 µl contained: 400 µg terminal labeled DNA (Example 11), 0.2 M sodium acetate pH 4.7 and 0.1 M $NaIO_4$. It was incubated for two hours at room temperature in the dark and the mixture was passed through a G 50 column equilibrated in 0.3 M potassium borate pH 9.0-9.3, fractions of 0.2 ml were collected. All radioactive fractions were combined in a total volume 1.2 ml. The DNA solution was made 0.4 M with one of the amino components (ε-aminocaproic acid, cysteamine, or 1,6-diaminohexane, using a stock solution of 1 M which was adjusted to pH 9.3), and was incubated in the dark for 90 minutes at room temperature.

The resulting Schiff base was reduced with $NaBH_4$ as follows: $NaBH_4$ freshly dissolved to 0.2 M in water (1 ml) to M was added in four portions over 30 minute intervals. The incubation was continued for a total of 3 hours. The salts and the excess of the amino component were removed by G 50 filtration in a column equilibrated in 0.4 M sodium acetate containing 1mM beta-mercaptoethanol, the DNA-containing fractions were then combined and stored over argon at -70°C. Before use, DNA was precipitated with ethanol and dissolved in the desired buffer.

Example 13

Activation of bromoacetic acid N-hydroxysuccinimide ester

The NHS (N-hydroxy succinimide) ester of bromoacetic acid was prepared as follows: 100 mmoles of (13.9 g) of bromoacetic acid were dissolved in 50 ml of anhydrous DMF, to this solution 100 mmoles (20.6 g) of N-N-Dicyclohexylcarbodiimide were added with stirring followed by 100 mmoles of N-hydroxysuccinimide (11.9 g adjusted for 100% purity), and the mixture was stirred for 6 hours at 37°C. The mixture was then placed for 2 hours at -20°C to accelerate the precipitation of hydroxyurea, which was removed by filtration. In th filtrate th DMF was removed under reduced pr ssur at 45°C and the active ester was recrystallized from 2-propanal.

Example 14

Brom acetylation of IgG

IgG (20 mg/ml) in 0.3M potassium borate buff r pH 9.9 was mixed with 0.06 vol of a 10 mg/ml solution of the NHS ester of bromoacetic acid (Example 13) in DMSO, and the mixture was gently mixed for 1 hour at room temperature. The sample was then dialyzed against 0.1 M NaCl 0.1M phosphate buffer pH 7.5.

Example 15

Synthesis of DNA-IgG Conjugates

1.6 mg/ml of bromoacetylated IgG (Example 14) in 0.3 M potassium borate buffer were incubated at room temperature under argon with a thio-substituted, end labeled DNA solution (Example 12) of 3 mg/ml for 2 hours. Mercaptoethanol 0.01 M was then added and the mixture was further incubated at the same temperature for 2 hours to quench the unreacted bromine residues. The solution was th n adsorbed on a Protein A column, and the unconjugated DNA was eluted with 1.0 M NaCl. The DNA-IgG conjugate and the unreacted IgG were eluted with isothiocyanate, and dialyzed against 0.1M phosphate buffer, pH 7.2 to remove isothiocyanate. The conjugat d IgG and the free IgG were then precipitated with ammonium sulfate 50%, the pellet dissolved in 1.0 ml phosphate buffer and the free IgG was separated from the conjugated IgG by fractionation on a Bio-Gel p-300 column equilibrated in .01M NaCl, 0.1M phosphate pH 7.2.

Example 16

Mercuration of pBR322

pBR322 DNA (100 µg) dissolved in 1 ml of 5mM sodium acetate pH 7.5 containing mercuric acetate (3 mg, .01 mmol) was reacted for 4 hours at 50°C according to a procedure of Dale et al (Nucl. Acid R s. 2:915, 1975). The 5-cytosine mercurated DNA was exhaustively dialyzed in 0.01 M Tris HCl, pH 7.5, containing 0.02 sodium chloride 2mM EDTA.

Example 17

Iodination of Mercurated pBR 322 DNA

To the mercurated DNA from the previous experiment in 1 ml 0.1M Tris HCl pH 7.5 was added 1 mg iodine using the procedure of Dal et al (Nucl. Acid R s. 2, 915, 1975). After reaction at 20°C for 2 hours the excess I_2 was extract d with chloroform and the iodinated DNA was dialyzed against 0.01m Tris HCl pH 7.5 containing 0.02M sodium chlorid and 2mM

EDTA. Th substituted DNA was analyz d by successiv digestion with N. crassa ndonucleas , snake venon phosphodiesterase DNAse, and E. coli alkaline phosphatase (H. Yamasaki et al, Cancer Res. 37:1389, 1977). The mixture was eluted through DE-52 amino cellulose, and the nucleotides were analyzed by reverse phase HPLC using authentic 5-iodo-2'-deoxyuridine as a standard.

Example 18

Reaction of 5-Iodocytosine pBR322 DNA with amines.

Example of reaction with 1,6-Diaminohexane.

To the iodinated DNA from the previous reaction dialyzed into 1 ml 0.1 M sodium borate was added 116 mg (1 mmol) diaminohexane. The reaction mixture was flushed with argon and heated at 100° for 2 hours. The aminohexyl substituted DNA is exhaustively dialyzed into 0.01 M Tris HCl pH 7.5.

Reaction conditions for aminocaproic acid, bis (2-aminoethane) disulfide and 6-amino-α-methyl-D-manno (Example 5) are essentially identical.

Example 19

Coupling of Amino and Carboxy-Substituted Nucleic Acids to Proteins or Amines using 1-Ethyl-3-diisopropyl-aminocarbodiimide (EDAC).

Example of Streptavidin Coupled DNA

To a solution containing amino-or-carboxy-end substituted DNA (Example 11) (50 µg) and 3H-labelled Streptavidin (50 µg) dissolved in 1 ml 0.01M NaCl pH 7.5 (HCl) was added 5 mg EDAC. The reaction was incubated 20 hours in the dark and DNA was precipitated by addition of 4 M $CaCl_2$ (0.03 ml). DNA was redissolved in 1 ml water and this procedure was repeated 2 more times to remove unbound protein. The protein-coupled DNA was affinity purified in an iminobiotin-sepharose affinity column (K. Hoffman et al, PNAS 77:4666 1980) and dialyzed against 10mM NaCl.

Example 20

N-Hydroxy Succinimide Activation of Carboxyhexyl-Substituted DNA and Coupling to Proteins or Amines.

Examples of Streptavidin Coupled DNA

Carboxy end substituted DNA (Example 19) (50 µg) was conv rted to the triethylamonium salt by shaking an aqueous solution with Dowex 50-WX (Et_3N+). The solution was lyophylized and th dried DNA was dissolv d in anhydrous dimethyl formamid (0.5 ml) to which was added dicycl hexylcarbodiimide (10.3 mg, 0.05 mol) and N-Hydroxysuccinimide (5.8 mg 0.05 Mol). After incubating at room temperature for 20 hours the reaction was centrifugated and the supernatant dialyzed for 2 hours into 10 mM NaCl. Streptavidin (50 µg) dissolved in 0.2 M borate, pH 8.5 (1 ml) was added to the N-hydroxysuccinimide activated DNA and the reaction was incubated 20 hours and dialyzed into 0.01M NaCl. The Streptaviden coupled DNA was purified by $CaCl_2$ precipitation and iminobiotin affinity chromatography as previously described.

Example 21

Reaction of DNA with Glyoxal

DNA (1 µg) (BAM insert from plasmid pDK14) was dissolved in 0.025 M glyoxal (0.2 ml) and heated at 100°C for 30 minutes in a sealed tube. The reaction was dialyzed against 10 mM NaCl. In order to ass ss degree of reaction on guanosine, a portion of the reaction was subjected to acid depurination by lowering the pH to 1.0 with HCl, and heating at 100°C for 30 minutes. The depurinated DNA was removed by elution through DE-52 amino cellulose and the eluted purines analyzed by HPLC on reverse phase. Comparison of peak heights of adenosine, guanosine and glyoxal-guanosine adduct (R. Shapiro et al, Biochem 5:2799, 1966) revealed that 70% of the guanosines had been substituted.

Example 22

N-biotinyl-4-amino-acetophenone

To a solution of biotin-N-hydroxysuccinimide ester (50 µg, 0.014 mmol) dissolved in 20 ml dimethylformamide (DMF) was added 4-aminophenylacetophenone (4.35 g, .03 mol) dissolved in 50 ml DMF and 100 ml 0.1 M borate buffer pH 8.5. After reaction at room temperature for 20 hours, the solvent was removed by rotary evaporation. The residual oil was triturated first with 0.1 N HCl and then with 5% sodium bicarbonate. The product was crystallized from ethanol.

Example 23

Biotinyl (4-aminophenyl)glyoxal

Selenium dioxide (0.75 g, 7 mmol) was dissolved in 4 ml dioxan containing 0.15 ml water. To this was added dropwis a solution of N-biotinyl-4-amino acetophenone (1.9 g, 7 mmol) dissolved in 5 ml dioxane. The reaction was refluxed for 3.5 hours aft r which

th mixtur was filtered and conc ntrated under vacuum. The crude product was purified by silica gel chromat graphy.

Example 24

1,N-Biotinyl-1,6-hexanediamine

Biotin-N-hydroxysuccinimide ester (1.0 g, 2.9 mmol) dissolved in dimethylformamide (5µm) was added to a solution of diaminohexane (1.15g, 10 mmol) in 0.1 M sodium borate (500 ml). After reacting at room temperature for 5 hours, the solution was rotary evaporated, redissolved in 10 ml water and chromatographed on Dowex 50 wx (H+). The column was washed with 50% aqueous methanol and the fraction eluted with triethylamine dissolved in 50% aqueous methanol (.3M) was collected. The evaporated residue was thoroughly triturated with ether and recrystallized from DMF/ether.

Example 25

CH_3-CO-CONH-$(CH_2)_6$-NH-Biotin

To a solution of pyruvic acid (.44 g, 5 mmol) cooled to 4°C, 20 ml anhydrous DMF was added isobutylchloroformated (0.64 g, 5 mmol) and tri-N-butylamine (1.43 g, 1.5 mmol). After 20 minutes at this temperature, an additional 1.4 g tri-N-butylamine was added and the mixture was added to a solution of 1,N-biotinyl-1,6-hexane diamine (Example 24) (.34 g, 1 mmol) dissolved in 30 ml DMF and 30 ml 0.1 M sodium borate. After reacting at 4°C for 1 hr. the mixture was allowed to stand at room temperature for an additional 20 hours and subsequently concentrated in vacuo. The mixture was purified by chromatography on silica gel and the product recrystallized from ethanol.

Example 26

CHO-CO-CONH-$(CH_2)_6$-NH-Biotin

Selenium dioxide (54 mg, 0.5 mmol) was dissolved in dioxane (0.5 ml) containing 25 µl water. A solution of CH_3-CO-CONH-$(CH_2)_6$-NH-Biotin (Example 25) (0.21 g 0.5 mmol) dissolved in 1 ml dioxane was added dropwise and the reaction was heated at 100° for 4 hours. The resultant precipitate was removed by centrifugation, washed with dioxane and the supernatant was concentrated in vacuo. The crude mixture was chromatographed on silica gel.

Example 27

Reaction of DNA with Biotinylated Glyoxal Derivatives

DNA (1 µg) as a triethylammonium salt was dissolved in 100 µl water. To this was added 100 µl of a solution of (N-biotinyl (4-aminophenyl)) glyoxal (0.05 M) or CHO-CO-CONH-$(CH_2)_6$-NH-Biotin (0.05M) in dimethylformamide. The mixture was heated at 100°C for 30 minutes in a sealed tube and subsequently dialyzed against 0.01 M NaCl. Extent of reaction was determined by acid depurification and HPLC assay of purine nucleosides, as described previously.

Example 28

Bromination of pBR 322 DNA

To a solution of pBR 322 DNA (100 µg) dissolv d in 0.5 M acetate buffer pH 5.5. was added bromin (5.5 µl, 0.1 mmol). The reaction was incubated at 60° for 30 hours and exhaustively dialyzed against 0.01 M NaCl.

Example 29

Reaction of Brominated pBR 322 DNA with Thiols.

Example of Reaction with Cysteamine and 3-Mercaptopropionic acid.

A solution of brominated pBR 322 DNA (500 µg) in 0.1 M borate pH 8.5 (1 ml) was incubated with ither cysteamine or 3-mercaptopropionic acid (20 mg) for 20 hours at room temperature under an argon atmosphere. The resultant amine-or carboxy- substituted DNA was dialyzed against 0.01 M NaCl.

Example 30

Reaction of Brominated pBR322 DNA with Amines.

Example of Reaction with 1,6-Diaminohexane

A solution of brominated pBR 322 DNA (100 µg) and 1 M of 1,6-diaminohexane (1ml) were heat d at 65° for 3 hours under an argon atmosphere. The resultant amine-sbustituted DNA was dialyzed against 0.1 M NaCl.

Example 31

Synth sis of a Protein Coupled to a Signal Generating Polynucleotide. Example of IgG Coupl d to Chemically Radio-labeled DNA.

Fd DNA was end lab ll d with UMP using termi-

nal transf rase under conditions described in Example 11. The end labelled DNA was derivatized with 2,4,5-trichloroanilin (Exampl 1) and reacted with DCTA-SH under identical conditions to those described in Example Ia. The end labelled, DCTA derivatized DNA was oxidized with sodium periodate, reacted with cysteamine and reduced with sodium borohydride as described in Example 12. This was in turn reacted with bromoacetylated IgG (Example 14) using conditions described in Example 15.

Example 32

Use of Bacteriophage M13 as Bridging Entity

Using techniques of recombinant DNA technology, an asymmetric DNA sequence can be inserted in the replicative (double-stranded form) of a single-stranded phage such as M13. One strand of the insert will be deficient in guanine residues. As a result of this insertion, two single-stranded phages will be obtained in both polarities, one containing the (G-) strand, i.e., no guanylate residues of the asymmetric sequence, the other containing the sequence complementary to the G(-) sequence, to be called the G(+) sequence.

The G(+) phage is used as the vector (bridging entity) for carrying a DNA probe of interest such as, for example, herpes simplex virus I DNA sequences.

The G(-) phage (signalling entity) is chemically reacted with a guanosine specific reagent, such as a 1,2-dicarbonyl reagent. The G(-) insert in the G(-) phage would not be modified because it lacks guanylate residues.

A general protocol for the preparation of single-stranded M13 would be as follows:

1. M13 mp8 rf (replicative form, double-stranded), is grown. It is cut with Hinc II, which leaves blunt ends.
2. pd(G-T)$_5$ and pd(A-C)$_5$ are provided and hybridized to form a perfect double-strand. The ends must be perfectly matched. In order to obtain this condition it is necessary to use high C_ot conditions for hybridization.
3. The hybrids are ligated in the presence of the restriction enzyme Rsa I. Rsa I recognizes the sequence GTAC, and hence will cut to leave blunt ends and proofread the ligation.
4. The ligation products are isolated. They are double-stranded poly d (G-T) poly d (A-C).
(Any complementary, repeating, low complexity sequence can be used. The subsequent modification and chemistries must be adjust d accordingly.)
5. Alkaline phosphatase is used to r mov 5' phosphat s.
6. Polynucleotide kinas and ^{32}P-ATP ar used to replace 5' nds with ^{32}P-phosphat s.
7. Th reaction mixtur is run over 15-20% nond naturing polyacrylamide gels to s parate the different size fragments.
8. Th fragm nts are located on gels by autoradiography.
9. The desired size bands are eluted out of the gel by cutting, mashing and then extracting the gel with high salt buffer. Fragments having 50-100 bp or larger are preferred.
10. DNA is concentrated by any of a numb r of possible techniques, such as ethanol precipitation, spermine precipitation, lyophilization, or the like.
11. The fragments are ready to be cloned into Hinc II-cut M13.
Using the standard cloning technique, the following sequence is performed:
   a. Fragments are ligated into M13;
   b. Cells (for example E. coli JM103) are transformed with the M13;
   c. Transformed cells are plated; and
   d. Recombinants are selected.
12. There are two possible routes for selection of recombinants:
   a. If a known size class has been inserted, plaques will be picked and sequenced to ch ck for the presence of insert.
   b. An alternative procedure is to shotgun all the sequences made in step 4 into M13. This protocol requires that many more clones b picked and then checked by sequencing.
13. Once a suitable clone has been obtained (M13 with the appropriate size sequence), the strand that gives GTGT, etc., in the single-strand replicating form will be selected. This clone is then used for further genetic engineering by inserting sequences from a variety of pathogens into the replicating form.
14. The strand that gives ACAC etc. in the replicating form is cloned in mass culture and chemically modified with a reporter (signal generation portion) that is specific for G's. Thus the G(-) phage is exhaustively reacted with the bifunctional reagent p-azidophenyl glyoxal (APG). The dicarbonyl moiety of APG reacts only with guanosine residues in single-stranded portions of th DNA. The insert lacking guanosine is not affected by this treatment.
15. The (G+) and derivatized (G-) DNAs are mixed in equimolar concentration and allowed to hybridize to target DNAs and to each other. Visualization of the hybrids is by standard signal reporting techniques.

Claims

1. A method of detecting in a sampl an analyte hav-

ing a molecularly recognizabl portion thereon, c mprising:

forming a complex comprising (1) said analyte bound to (2) a molecular bridging entity comprising a portion capable of recognizing and binding to said molecularly recognizable analyte portion, and a portion comprising a polynucleotide sequence; and (3) a signalling entity comprising a recognition portion capable of complexing to said polynucleotide portion of said bridging entity, and a signal generating portion with the proviso that when said analyte is a polynucleotide, the signal generating portion is not an enzyme that is covalently linked to said recognition portion; and

detecting a signal provided by said signal generating portion present in said complex.

2. The method according to Claim 1, characterized in that said analyte is immobilized.

3. The method according to Claim 1, characterized in that said analyte is a microorganism or fragment thereof which is selected from the group consisting of a virus, a viral component, a bacterium, a bacterial component, a cell, a cellular component and a pathogen or non-pathogen or a component thereof.

4. The method according to Claim 3, characterized in that said molecularly recognizable portion on said microorganism is selected from the group consisting of an RNA and DNA nucleotide, oligonucleotide sequence, polynucleotide sequence, peptide, polypeptide protein, antigen, antibody, lectin, saccharide, hormone, ligand, enzyme inhibitor, enzyme cofactor, enzyme, and substrates and receptors thereof.

5. The method according to Claim 1, characterized in that said bridging entity recognizing portion is selected from the group consisting of an RNA or DNA nucleotide, an oligonucleotide sequence, polynucleotide sequence, peptide, polypeptide, and protein, and an antigen, a polyclonal antibody, a monoclonal antibody, a saccharide, a lectin, a hormone, a ligand, an enzyme inhibitor, an enzyme cofactor, an enzyme, and substrates and receptors thereof.

6. The method according to Claim 1, characterized in that said bridging entity polynucleotide sequ nc is sel cted from th group consisting of a poly deoxy-G, poly deoxy-C, poly d oxy-T or poly deoxy-A sequence, or any poly-ribo or -deoxyribo purine, pyrimidin or analog, a gene product or fragment thereof, or a s qu nc substantially comprising adenin residues, a sequ nce substantially comprising a residue selected from the group consisting of guanine, cytosine, thymin , uracil, guanosin .

7. The method of claim 1 characterized in that said bridging entity recognizing portion is covalently bound to said bridging entity polynucleotid sequence.

8. The method according to Claim 1, characterized in that said bridging entity is selected from the group consisting of a single-stranded, double stranded or partially double-standed circular DNA polymer, a circular DNA polymer d rived from a filamentous phage, an M13 phage or a variant thereof, a DNA molecule comprising a polynucleotide sequence complementary to part or all of a gene sequence of a nucleic acid-containing organism.

9. The method according to Claim 1, characterized in that said signalling entity receptor is a polynucleotide sequence selected from the group comprising a poly deoxy C, poly deoxy G, poly deoxy A, poly deoxy T sequence, a repeating sequence of low complexity, a sequence portion substantially comprising cytosine residues or guanosine residues, and a sequence coding for a gene product or fragment thereof.

10. The method according to Claim 1, charact rized in that said signalling entity is selected from the group consisting of a single stranded, double stranded, or partially double-stranded polynucleotide polymer, a modified naturally occurring DNA, a polynucleotide polymer derived from a T (even) phage, a modified DNA carrying a cloned insert, a polymer derived from a filamentous phage, M13 phage or a variant thereof, and a polymer derived from a circular DNA molecule covalently attached to a non radio-labelled signal generating moiety.

11. The method according to Claim 1, characterized in that said signal generating portion is selected from the group consisting of a radioactive moiety, an enzyme, a lectin, an antibody, an antigen, a biotin moiety, a saccharide, a fluorogenic compound, an electron dense compound, a polynucleotide sequence capable of recognizing a signal-containing moiety, a compound capable of binding to an insoluble phase, a latex particle, a resin and a bacterium.

12. The method according to Claim 1, characterized in that said detecting step is selected from the group consisting of a radioactivity measurement, an enzymatic reaction, a fluorescence measure-

ment, an lectron microscopic measurement, an antibody/antigen complexation reaction, a bi tin and biotin binding moiety compl xation reaction, an avidin-streptavidin complexation reaction, an electron density measurement, a saccharide and lectin complexation reaction, a binding step on an insoluble phase, and complexation between a signalling entity comprising a cloned insert on a naturally occurring modified DNA, and the bridging moiety, followed by binding a modified lectin to said signalling entity.

13. A polynucleotide sequence covalently attached to an antibody.

14. The sequence of Claim 13 wherein said antibody is monoclonal.

15. A polynucleotide sequence covalently attached to a lectin.

16. A polynucleotide sequence covalently attached to a saccharide having up to 20 saccharide units.

17. A polynucleotide sequence covalently attached to receptor.

18. A polynucleotide sequence covalently attached to a hormone.

19. A kit useful for the detection of an analyte (A) having a molecularly recognizable portion thereof, comprising:
I) a carrier being compartmentalized to receive in close confinement therein therein one or more container means;
II) a first container means containing a molecular bridging entity (B) having thereon:
(i) a portion capable of recognizing said molecularly recognizable portion on said analyte (A); and
(ii) a portion comprising a polynucleotide sequence;
III) a second container means containing a signalling entity (C) having thereon:
(i) a polynucleotide portion capable of annealing to said polynucleotide portion of said bridging entity (B) thereby to form a stable polynucleotide hybrid; and
(ii) a signal generating portion with the proviso that when said analyte is a polynucleotide, the signal generating portion is not an enzym that is covalently linked to said recognition portion; and
IV) oth r containerm ans, wh r appropriat , containing molecular entiti s n cessary or us ful in d tecting, making d tectable or enhancing the signal of the said signal generating portion of said signalling entity (C).

20. The method according to claim 11 wherein said fluorog nic compound is directly or indirectly linked to said signalling entity.

21. The method according to claims 1 or 2, characterized in that said forming step comprises contacting said analyte with said molecular bridging entity to form a first complex and thereafter contacting said first complex with said signalling entity to form a subsequent complex.

22. The method according to claims 1 or 2, characterized in that said forming step comprises contacting said molecular bridging entity with said signalling entity to from a first complex and thereafter contacting said first complex with said analyte to form a subsequent complex.

23. The method according to claim 2 further comprising a washing step after formation of the first complex, or after formation of the subsequent complex, or after each complex formation.

Patentansprüche

1. Verfahren zum Nachweis eines Analyten mit einem erkennbaren Molekülanteil in einer Probe, umfassend:
Bildung eines Komplexes, umfassend (1) d n Analyten, der an (2) eine molekulare brückenbildende Einheit gebunden ist, die einen Anteil umfaßt, der den erkennbaren Molekülanteil des Analyten erkennen und binden kann, und ein n Anteil, der eine Polynucleotidsequenz umfaßt; und (3) einen signalgebenden Anteil, der einen Erkennungsanteil umfaßt, der mit dem Polynucleotidanteil der brückenbildenden Einheit ein n Komplex bilden kann, und einen signalerzeugenden Anteil, mit der Maßgabe, daß, falls der Analyt ein Polynucleotid ist, der signalerzeugende Anteil kein Enzym ist, das kovalent an den Erk nnungsanteil gebunden ist; und
Nachweis eines Signals, das von dem in d m Komplex vorhandenen signalerzeugenden Anteil geliefert wird.

2. Verfahren nach Anspruch 1, dadurch gekennzeichnet, daß der Analyt immobilisiert ist.

3. Verfahren nach Anspruch 1, dadurch gekennzeichn t, daß d r Analyt ein Mikroorganismus oder ein Fragment davon ist, ausgewählt aus einem Virus, inem viralen Bestandteil, einem Bakterium, einem bakteriellen Bestandteil, in r Zelle, einem zellulären B standteil und ein m Pa-

thogen oder Nicht-Pathogen oder ein m Bestandteil davon.

4. Verfahren nach Anspruch 3, dadurch gekennzeichnet, daß der erkennbare Mol külanteil auf dem Mikroorganismus ausgewählt ist aus einem RNA- und DNA-Nucleotid, einer Oligonucleotidsequenz, Polynucleotidsequenz, einem Peptid, Polypeptid, Protein, Antigen, Antikörper, Lectin, Saccharid, Hormon, Liganden, Enzyminhibitor, Enzymcofaktor, Enzym und Substraten und Rezeptoren davon.

5. Verfahren nach Anspruch 1, dadurch gekennzeichnet, daß der die brückenbildende Einheit erkennende Anteil ausgewählt ist aus einem RNA- oder DNA-Nucleotid, einer Oligonucleotidsequenz, Polynucleotidsequenz, einem Peptid, Polypeptid, Protein, Antigen, polyclonalen Antikörper, monoclonalen Antikörper, Saccharid, Lectin, Hormon, Liganden, Enzyminhibitor, Enzymcofaktor, Enzym und Substraten und Rezeptoren davon.

6. Verfahren nach Anspruch 1, dadurch gekennzeichnet, daß die Polynucleotidsequenz der brückenbildenden Einheit ausgewählt ist aus einer Polydesoxy-G-, Polydesoxy-C-, Polydesoxy-T- oder Polydesoxy-A-Sequenz, oder einem beliebigen Polyribo- oder -desoxyribopurin oder -pyrimidin oder Analogen, einem Genprodukt oder Fragment davon, einer Sequenz, die im wesentlichen Adeninreste umfaßt, und einer Sequenz, die im wesentlichen Reste umfaßt, ausgewählt aus Guanin, Cytosin, Thymin, Uracil oder Guanosin.

7. Verfahren nach Anspruch 1, dadurch gekennzeichnet, daß der die brückenbildende Einheit erkennende Anteil kovalent an die Polynucleotidsequenz der brückenbildenden Einheit gebunden ist.

8. Verfahren nach Anspruch 1, dadurch gekennzeichnet, daß die brückenbildende Einheit ausgewählt ist aus einem einzelsträngigen, doppelsträngigen oder teilweise doppelsträngigen zirkulären DNA-Polymer, einem zirkulären DNA-Polymer, das von einem filamentösen Phagen, einem M13-Phagen oder einer Variante davon stammt, einem DNA-Molekül, das eine Polynucleotidsequenz umfaßt, die zu einem Teil einer G nsequenz oder iner gesamt n Gensequenz ein s eine Nucleinsäure enthaltend n Organismus komplem ntär ist.

9. Verfahren nach Anspruch 1, dadurch gekennz ichnet, daß der di signalgebende Einheit erk nnende Anteil ein Polynucleotidsequenz ist, ausgewählt aus einer Polydesoxy-C-, Polydesoxy-G-, Polyd soxy-A-, Polydesoxy-T-Sequenz, einer sich wiederholenden Sequenz geringer Komplexität, ein m Sequenzanteil, der im wesentlichen Cytosinreste oder Guanosinreste umfaßt, und einer Sequenz, die ein Genprodukt oder Fragment davon codiert.

10. Verfahren nach Anspruch 1, dadurch gekennzeichnet, daß der die signalgebende Einh it erkennende Anteil ausgewählt ist aus einem einzelsträngigen, doppelsträngigen oder teilweis doppelsträngigen Polynucleotidpolymer, einer modifizierten, natürlich vorkommenden DNA, ein m Polynucleotidpolymer, das von einem (geradzahligen) T-Phagen stammt, einer modifizierten DNA, die eine clonierte Insertion trägt, einem Polymer, das von einem filamentösen Phag n, M13-Phagen oder einer Variante davon stammt, und einem Polymer, das von einem zirkulären DNA-Molekül stammt, das kovalent an ein nichtradioaktiv markierte signalerzeugende Einheit geknüpft ist.

11. Verfahren nach Anspruch 1, dadurch gekennzeichnet, daß der signalerzeugende Anteil ausgewählt ist aus einer radioaktiven Einheit, ein m Enzym, einem Lectin, Antikörper, Antigen, Biotinanteil, Saccharid, einer fluorogenen V rbindung, einer Verbindung mit hoher Elektron ndichte, einer Polynucleotidsequenz, die einen signalenthaltenden Anteil erkennen kann, ein r Verbindung, die an eine unlösliche Phase bind n kann, einem Latexpartikel, einem Harz und einem Bakterium.

12. Verfahren nach Anspruch 1, dadurch gekennzeichnet, daß der Nachweisschritt ausgewählt ist aus einer Radioaktivitätsmessung, einer nzymatischen Reaktion, einer Fluoreszenzmessung, einer elektronenmikroskopischen Messung, iner Antikörper/Antigenkomplexierungsreaktion, einer Komplexierungsreaktion zwischen in m Biotin und einem biotinbindenden Anteil, iner Avidin-Streptavidin-Komplexierungsreaktion, einer Elektronendichtemessung, einer Komplexierungsreaktion zwischen einem Saccharid und einem Lectin, einem Bindungsschritt an ein unlösliche Phase, und einer Komplexierungsreaktion zwischen einer signalgebenden Einheit, die eine clonierte Insertion auf einer natürlich vorkommend n, modifizierten DNA umfaßt, und der brückenbildenden Einheit und im Anschluß daran di Bindung ines modifiziert n Lectins an die signalgebende Einheit.

13. Polynucleotidsequenz, di kovalent mit in m

Antikörper verknüpft ist.

14. Sequenz nach Anspruch 13, wobei der Antikörper ein monoclonaler Antikörper ist.

15. Polynucleotidsequenz, die kovalent mit einem Lectin verknüpft ist.

16. Polynucleotidsequenz, die kovalent mit einem Saccharid mit bis zu 20 Saccharideinheiten verknüpft ist.

17. Polynucleotidsequenz, die kovalent mit einem Rezeptor verknüpft ist.

18. Polynucleotidsequenz, die kovalent mit einem Hormon verknüpft ist.

19. Kit, verwendbar zum Nachweis eines Analyten (A) mit einem erkennbaren Molekülanteil, umfassend:
I) einen Träger, der zur Aufnahme von einem oder mehreren Behältern auf engem Raum aufgeteilt ist;
II) einen ersten Behälter, der eine molekulare brückenbildende Einheit (B) enthält, die
(i) einen Anteil, der den erkennbaren Molekülanteil auf dem Analyten (A) erkennen kann; und
(ii) einen eine Polynucleotidsequenz umfassenden Anteil umfaßt;
III) einen zweiten Behälter, der eine signalgebende Einheit (C) enthält, die
(i) einen Polynucleotidanteil, der den Polynucleotidanteil der brückenbildenden Einheit (B) anlagern kann, wodurch ein stabiles Polynucleotidhybrid gebildet wird; und
(ii) einen signalerzeugenden Anteil umfaßt, mit der Maßgabe, daß, falls der Analyt ein Polynucleotid ist, der signalerzeugende Anteil kein Enzym ist, das kovalent an den Erkennungsanteil gebunden ist; und
IV) falls erforderlich weitere Behälter, die molekulare Einheiten enthalten, die notwendig oder nützlich sind, das Signal des signalerzeugenden Anteils der signalgebenden Einheit (C) nachzuweisen, nachweisbar zu machen oder zu erhöhen.

20. Verfahren nach Anspruch 11, wobei die fluorogene Verbindung direkt oder indirekt mit der signalgebenden Einheit verbunden ist.

21. Verfahren nach Anspruch 1 oder 2, dadurch gekennzeichnet, daß der Schritt der Bildung das Inkontaktbringen des Analyten mit der molekularen brückenbildenden Einheit zur Bildung eines ersten Komplexes umfaßt und im Anschluß daran das Inkontaktbringen des ersten Komplexes mit der signalgebenden Einheit zur Bildung eines weiteren Komplexes.

22. Verfahren nach Anspruch 1 oder 2, dadurch gekennzeichnet, daß der Schritt der Bildung das Inkontaktbringen der molekularen brückenbildenden Einheit mit der signalgebenden Einheit zur Bildung eines ersten Komplexes umfaßt und im Anschluß daran das Inkontaktbringen des ersten Komplexes mit dem Analyten zur Bildung eines weiteren Komplexes.

23. Verfahren nach Anspruch 2, außerdem umfassend einen Waschschritt nach der Bildung des ersten Komplexes oder nach der Bildung des weiteren Komplexes oder nach jeder Komplexbildung.

Revendications

1. Procédé de détection dans un échantillon d'un analyte contenant une portion reconnaissable du point de vue moléculaire, comprenant les étapes de :
formation d'un complexe comprenant (1) ledit analyte lié à (2) une entité moléculaire formant un pont constituée d'une portion capable de reconnaître à la portion d'analyte reconnaissable du point de vue moléculaire et de s'y lier, et d'une portion constituée d'une séquence polynucléotidique ; et (3) une entité produisant un signal, constituée d'une portion de reconnaissance capable de se complexer à ladite portion polynucléotidique de ladite entité formant un pont, et une portion générant un signal à la condition que, lorsque ledit analyte est un polynucléotide, la portion générant un signal ne soit pas une enzyme liée par covalence à ladite portion de reconnaissance ; et
détection d'un signal émis par ladite portion générant un signal présente dans ledit complexe.

2. Procédé selon la revendication 1, caractérisé en ce que ledit analyte est immobilisé.

3. Procédé selon la revendication 1, caractérisé en ce que ledit analyte est un micro-organisme ou un fragment de celui-ci, qui est choisi dans le groupe constitué d'un virus, d'un composant viral, d'une bactérie, d'un composant bactérien, d'un cellule, d'un composant cellulaire et d'un agent pathogène ou non pathogèn ou d'un composant d celui-ci.

4. Procédé selon la revendication 3, caract´risé en

ce que ladit portion reconnaissable du point de vue moléculair dans ledit microorganisme st choisie dans le groupe constitué d nucléotide d'ARN et d'ADN, s´quence oligonucléotidiqu , séquence polynucléotidique, peptide, polypeptide, protéine, antigène, anticorps, lectine, saccharide, hormone, ligand, inhibiteur d'enzyme, cofacteur d'enzyme, enzyme, et substrats et récepteurs de ceux-ci.

5. Procédé selon la revendication 1, caractérisé en ce que ladite portion reconnaissant de l'entité formant un pont est choisie dans le groupe constitué d'un nucléotide d'ARN et d'ADN, d'une séquence oligonucléotidique, d'une séquence polynucléotidique, d'un peptide, d'un polypeptide et d'une protéine, et d'un antigène, d'un anticorps polyclonal, d'un anticorps monoclonal, d'un saccharide, d'une lectine, d'une hormone, d'un ligand, d'un inhibiteur d'enzyme, d'un cofacteur d'enzyme, d'une enzyme, et de substrats et récepteurs de ceux-ci.

6. Procédé selon la revendication 1, caractérisé en ce que la séquence polynucléotidique de l'entité formant un pont est choisie dans le groupe constitué d'une séquence polydésoxy-G, polydésoxy-C, polydésoxy-T ou polydésoxy-A ou tout polyribo- ou polydésoxyribopurine, pyrimidine ou analogue, d'un produit de gène ou un fragment de celui-ci, ou d'une séquence substantiellement constituée de résidus adénine, d'une séquence substantiellement constituée d'un résidu choisi dans le groupe constitué de guanine, cytosine, thymine, uracile ou guanosine.

7. Procédé selon la revendication 1, caractérisé en ce que ladite portion de reconnaissance de l'entité formant un pont est liée par covalence à ladite séquence polynucléotidique de l'entité formant un pont.

8. Procédé selon la revendication 1, caractérisé en ce que ladite entité formant un pont est choisie dans le groupe constitué d'un polymère d'ADN circulaire monocaténaire, bicaténaire ou partiellement bicaténaire, un polymère d'ADN circulaire dérivé d'un phage filamenteux, d'un phage M13 ou d'un variant de ceux-ci, ou d'une molécule d'ADN constituée d'une séquence polynucléotidique complémentaire d'une partie ou de la totalité d'une séquence de gène d'un organisme cont nant de l'acide nucléique.

9. Procédé selon la revendication 1, caractérisé en ce qu ladite portion de r connaissanc de l'entité produisant un signal est une séquence polynucléotidique choisi dans le groupe constitué d'un séquence polydésoxy-C, polydésoxy-G, polydésoxy-A, polyd´s xy-T, d'un séquenc de répétition de faible compl xité, d'un portion de séquence substantiellem nt constitu´ de résidus cytosine ou de résidus guanosine, et d'une séquence codant pour un produit de gène ou un fragment de celui-ci.

10. Procédé selon la revendication 1, caractérisé en ce que ladite portion de reconnaissance de l'entité produisant un signal est choisie dans l groupe constitué d'un polymère polynucléotidique monocaténaire, bicaténaire ou partiellement bicaténaire, d'un ADN naturel modifié, d'un polymère polynucléotidique dérivé d'un phag T (lisse), d'un ADN modifié portant un insert cloné, d'un polymère dérivé d'un phage filam nteux, d'un phage M13 ou d'un variant de ceux-ci, et d'un polymère dérivé d'une molécule d'ADN circulaire fixé par covalence à un fragment générant un signal non radiomarqué.

11. Procédé selon la revendication 1, caractérisé en ce que ladite portion générant un signal est choisie dans le groupe constitué d'un fragm nt radioactif, d'une enzyme, d'une lectine, d'un anticorps, d'un antigène, d'un fragment de biotine, d'un saccharide, d'un composé fluorogène, d'un composé dense aux électrons, d'une séquence polynucléotidique capable de reconnaître un fragment contenant un signal, d'un compos´ capable de fixer sur une phase insoluble, un particule de latex, une résine et une bactérie.

12. Procédé selon la revendication 1, caractérisé en ce que ladite étape de détection est choisi dans le groupe constitué d'une mesure de la radioactivité, d'une réaction enzymatique, d'une m sure de la fluorescence, d'une mesure au microscope électronique, d'une réaction de complexation anticorps/antigène, d'une réction de complexation de biotine et de fragment fixant la biotine, d'une réaction de complexation avidine-streptavidine, d'une mesure de densité aux électrons, d'une réaction de complexation saccharidel ctine, d'une étape de fixation sur une phase insolubl , et d'une complexation entre une entité produisant un signal constituée d'un insert cloné sur un ADN naturel modifié, et le fragment formant un pont, suivie de la fixation d'une lectine modifiée sur ladite entité produisant un signal.

13. Séquence polynucléotidique fixée par covalence sur un anticorps.

14. Séqu nc selon la r vendication 13, dans laquel l ledit anticorps st monoclonal.

15. Séquenc polynucléotidique fixé par covalenc sur un l ctin .

16. Séquence polynucléotidique fixée par covalence à un saccharide ayant jusqu'à 20 unités saccharidiques.

17. Séquence polynucléotidique fixée par covalence sur un récepteur.

18. Séquence polynucléotidique fixée par covalence sur une hormone.

19. Kit pouvant être utilisé pour la détection d'un analyte (A) ayant une portion reconnaissable du point de vue moléculaire, comprenant :

I) un support séparé en compartiments pour recevoir, étroitement renfermés à l'intérieur, un ou plusieurs dispositifs de conditionnement ;

II) un premier dispositif de conditionnement contenant une entité moléculaire formant un pont (B) contenant :

(i) une portion capable de reconnaître ladite portion reconnaissable du point de vue moléculaire sur ledit analyte (A) ; et

(ii) une portion constituée d'une séquence polynucléotidique ;

III) un second dispositif de conditionnement contenant une entité signal (C) ayant sur elle :

(i) une portion polynucléotidique capable de s'hybrider à ladite portion polynucléotidique de ladite entité formant un pont (B) pour former ainsi un hybride polynucléotidique stable ; et

(ii) une portion générant un signal, à la condition que, quand ledit analyte est un polynucléotide, la portion générant un signal ne soit pas une enzyme liée par covalence à ladite portion de reconnaissance ; et

IV) d'autres moyens de conditionnement, si nécessaire, contenant les entités moléculaires nécessaires ou utiles pour détecter, rendre détectable ou augmenter le signal de ladite portion générant un signal de ladite entité produisant un signal (C).

20. Procédé selon la revendication 11, dans lequel ledit composé fluorogène est directement ou indirectement lié à ladite entité produisant un signal.

21. Procédé selon les revendications 1 ou 2, caractérisé en ce que ladite étap d formation comprend la mise n contact dudit analyte av c ladite entité moléculaire formant un pont, pour former un premier complexe, puis la mis n contact dudit premi r complexe av c ladit entité produisant un signal pour form r un s cond compl xe.

22. Procédé selon les revendications 1 ou 2, caractérisé en ce que ladite étape de formation comprend la mise en contact de ladite entité moléculaire formant un pont avec ladite entité produisant un signal pour former un premier complexe, puis la mise en contact dudit premier complexe avec ledit analyte pour former un second complexe.

23. Procédé selon la revendication 2, comprenant en outre une étape de lavage après la formation du premier complexe, ou après la formation du second complexe, ou après la formation de chacun des complexes.

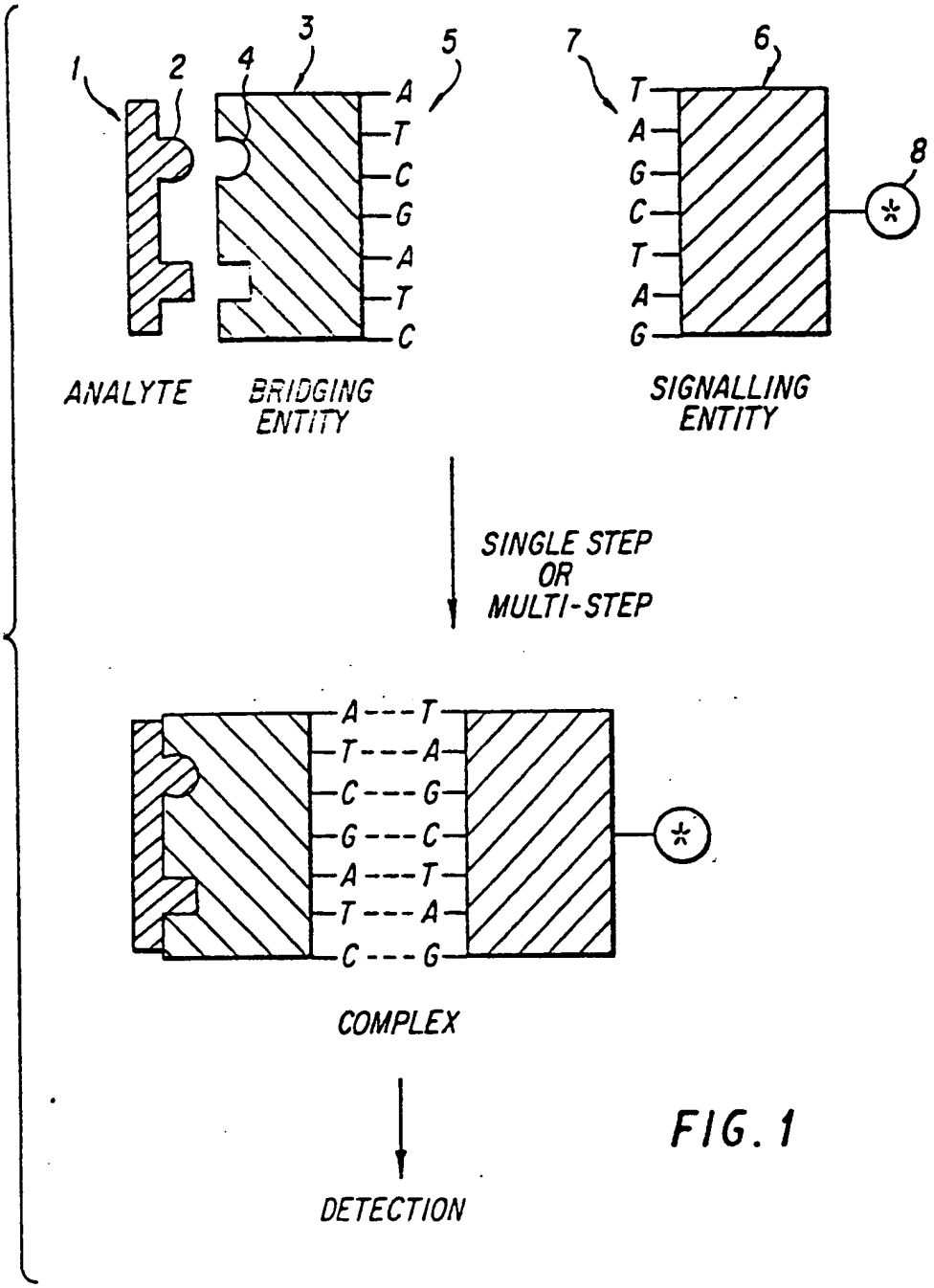
1
2
3
4
5
A
T
C
G
A
T
C
7
6
T
A
G
C
T
A
G
8
ANALYTE
BRIDGING ENTITY
SIGNALLING ENTITY
SINGLE STEP OR MULTI-STEP
A---T
T---A
C---G
G---C
A---T
T---A
C---G
COMPLEX
DETECTION

FIG. 1

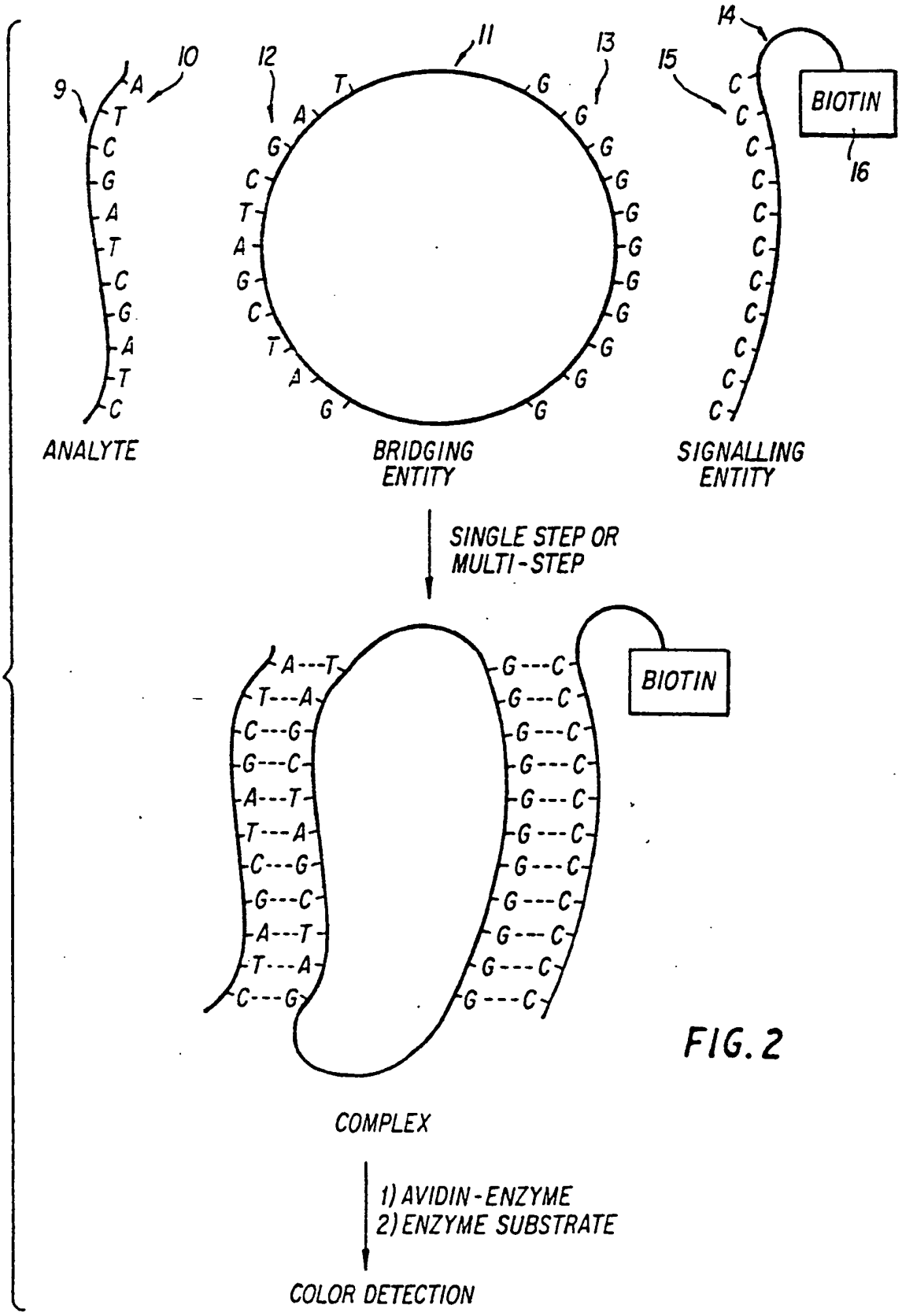
9
10
A
T
C
G
A
T
C
G
A
T
C
ANALYTE
12
11
13
T
A
G
C
T
A
G
C
T
A
G
G
G
G
G
G
G
G
G
G
G
G
BRIDGING ENTITY
14
15
C
C
C
C
C
C
C
C
C
C
C
BIOTIN
16
SIGNALLING ENTITY
SINGLE STEP OR MULTI-STEP
A---T
T---A
C---G
G---C
A---T
T---A
C---G
G---C
A---T
T---A
C---G
G---C
G---C
G---C
G---C
G---C
G---C
G---C
G---C
G---C
G---C
G---C
BIOTIN
COMPLEX
1) AVIDIN-ENZYME
2) ENZYME SUBSTRATE
COLOR DETECTION

FIG. 2